

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 04-25-02
Searcher: Boyle, E 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CON

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2002, 18:41:36 ; Search time 2503.91 seconds

Title: US-09-115-660-1

Sequence: 1 TTGGCCCCGAGCTCTTCAT.....AAAAAAAAAAAAAAAA 988

Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 359342

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 08

listing first 45 summaries

Database :

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32:	em_hfq_ph:	*
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34:	em_hfq_inv:	*

Third, NO, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

1	983	100.0	983	6	AR0444575	AR0444575, Sequence
2	983	100.0	983	6	AR1575660	AR1575660, Sequence
3	845.2	86.0	2460	8	IL1035436	IL1035436, Transcription
4	585	59.5	588	6	AX244978	AX244978, Sequence
5	243.6	24.8	786	8	IR0243191	IR0243191, Transcription
6	240.6	24.5	1039	8	IL1XYL1	IL1XYL1, Transcription
7	239	24.3	1123	6	B00068695	B00068695, Sequence
8	239	24.3	1123	6	IL163416	IL163416, Sequence
9	214.6	21.8	2202	8	AP246830	AP246830, Transcription
10	214.6	21.8	928	8	IV1012718	IV1012718, Transcription
11	205	20.9	1195	6	E28869	E28869, Sequence
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13	203.4	20.7	576	1	SC1292317	SC1292317, Sequence
14	203.4	20.7	2208	8	CEMXB2	CEMXB2, Sequence
15	202.2	20.6	40476	1	SC3737	SC3737, Sequence
16	200.2	20.4	1623	8	APB140X1	APB140X1, Sequence
17	199.8	20.3	1767	1	SPXY11	SPXY11, Sequence
18	199.6	20.3	4951	6	AP2443	AP2443, Sequence
19	199.6	20.3	4981	6	STMX1NB	STMX1NB, Sequence
20	199.4	20.3	1640	8	CE1XYL1AVNS	CE1XYL1AVNS, Sequence
21	199.2	20.3	1008	1	AF194025	AF194025, Sequence
22	199.2	20.3	1268	1	CEMXB7	CEMXB7, Sequence
23	194.8	19.8	2015	8	CEMXA1	CEMXA1, Sequence
24	194.6	19.8	695	8	CNS01075	CNS01075, Sequence
25	191.6	19.5	1020	8	IL1XYN1GNA	IL1XYN1GNA, Sequence
26	190	19.3	1015	6	AR055687	AR055687, Sequence
27	190	19.3	1075	8	SE7387	SE7387, Transcription
28	188.2	19.1	514	6	E28872	E28872, Sequence
29	187.8	19.1	2196	1	U01242	U01242, Sequence
30	186.4	19.0	1074	1	AP158618	AP158618, Sequence
31	186	18.9	2009	8	AR004085	AR004085, Sequence
32	185	18.8	1057	6	E02181	E02181, Sequence
33	183.8	18.7	1991	8	IFU218895	IFU218895, Sequence
34	183.4	18.7	1051	6	E02180	E02180, Sequence
35	181.8	18.5	1281	6	AR149835	AR149835, Sequence
36	179	18.2	1080	1	SSXMG	SSXMG, Sequence
37	171.8	17.5	5272	6	A22913	A22913, Sequence
38	171.6	17.5	617	12	STNXYLAN	STNXYLAN, Sequence
39	170.2	17.3	1579	1	AP120156	AP120156, Sequence
40	168.4	17.1	675	6	A25407	A25407, Sequence
41	168.4	17.1	1008	1	STMX1NC	STMX1NC, Sequence
42	168.4	16.9	37420	1	SC111	SC111, Sequence
43	165.2	16.8	516	6	A22805	A22805, Sequence
44	165.2	16.8	927	6	AR100156	AR100156, Sequence
45	165.2	16.8	927	6	AR137846	AR137846, Sequence

Result	Query	Post Position
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	100.0% Prod. No. 1, Box 243; Post Local Similarity	

[illegible]

DB	236	ACGGTACTTTCACCTGACTACTGAACGATGGCGACAGCGCCCGCTACGTAACCAATGGCT	294
QY	215	AAGCGCGGACCTACAGATATGACTTGGGAGATGGCGGTAAATCTCGTGGTGGAAAGGCT	274
DB	295	CGCGCGGCGTACTTCGCGCTCACTGGGCTCCAACTGGGGCAACTTTCGTGGCGGAAAGAT	354
QY	275	GGACGCGGACGCTTGAAAGCAAGACGACGACCTGATTGAGGGGTCTTTCAGCGGCAACGAGA	344
DB	355	GCGTACGCGGCAAGCAAGAACGATGATCACTTCTTCGGGAACTATTAATCTTAAAGGATA	414
QY	335	ACATATATCTTCGGCTTACGGTTGGAGCGCGCAACGCGGCTGCTGCTGCTAGTAAATATCGTGG	394
DB	415	ATACGTACTTCTCGGCTAGCGGCTGGTTCGCGACCGCCCTTAATCGATAGTAATATGCTGG	474
QY	395	AAATATCTTGGACATATATCTCTTCCTTCGCGGTCTACCGATTAAGTAATCTTGAGTATGG	454
DB	475	GGAAATCTTGGACATCAACGCTTCGACGCGCGCGCAACCTGGAGGAGATATCTATCTGG	534
QY	455	ACGTATGATCATCTGATCTGGGTAAGACGACCTCGGGCTGACATGACCTATATATATGGATA	514
DB	535	ATGCGTAGGCTTACCAACATTTATCGGCAACGACGAGCGGTCAATATGGTATATATGGATA	594
QY	515	CGCAACCTCTCGACCAATATCTGGTGGGTGCTTCGAGGACAGCGCAATATATGAGGCT	574
DB	595	CGCGCACTTTTACGATAGTCTGCTGCGCGCGGCAACGACGCGGTGGAGTGGCTGGGATA	654
QY	575	ATACGGGCTGCTACTTCGACGCGCTGGGCTCGCGCTGGCTTTATATCTCAATATATGACACT	634
DB	655	ACACGCGCAACATCTTCAACCTTCGCTGGGCTCAGCAAGCGCTGACCTTCCTCAAGAGATAG	711
QY	635	ACTTACCAATCTGCTGCAACGAGCGGCTACTTCGACGAGCGGCTATGCTCGATATATGCT	692
DB	712	ATTATCAATATCTTGGTGGCGGAGGGTTACTTTAGCTCTGACTTCTGCTGCTGATATATGCT	769
RESULT	6		
LOCUS	HEXYL1		
DEFINITION	H.INSOLENS XYL1 mRNA for endoxylanase.	1039 bp	mRNA
ACCESSION	X76047		linear
VERSION	X76047.1	GI:505260	
KEYWORDS	endoxylanase; xyl1 gene.		
SOURCE	Humicola insolens.		
ORGANISM	Humicola insolens.		
REFERENCE	Endo-Patai, Fungii: Ascomycota; mitosporic Ascomycota; Humicola.		
AUTHORS	1 (bases 1 to 1039)		
TITLE	Dalboe, H.		
JOURNAL	Submitted (04-NOV-1993) H. Dalboe, Madsen GeneExpress, Novo		
REFERENCE	Nordisk A/S, Symion, Frueljeveve) 3, 2100 Copenhagen O.E. DENMARK		
AUTHORS	2 (bases 1 to 1039)		
TITLE	Dalboe, H. and Holst-Hansen, H. P.		
	A novel method for efficient expression cloning of animal enzyme		
	genes		
JOURNAL	Mol. Gen. Genet. 243 (3), 253-260 (1994)		
FEATURES	94247364		
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	/db_xref "GI:505261"		
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[illegible]

[illegible]

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Run on:      April 27, 2002, 18:44:41 : Search time 322.92 Seconds
              (without alignments)
              526.455 Million cell updates/sec
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Title: US-09-115-660-1
Port of: 003

Sequence: 1 TCGGCCCGACGCTTGCAT.....AAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	length	DB	ID	Description
1	983	100.0	983	17	AA040742	Xylinase coding se
2	983	100.0	983	17	AA043010	Endo-1,4-beta-D-xy
3	585	59.5	588	22	AA043813	lignin-encoding Therm
4	374	58.0	678	22	AA017927	Thermomyces lanugi
5	239	24.3	1123	15	AA094952	Humicola insolens
6	239	24.3	1123	16	AA074058	Humicola xylinase
7	205	20.9	1195	20	AA028864	Streptomyces oliva
8	205	20.9	1195	20	AA028865	Streptomyces oliva
9	199.6	20.3	851	18	AA063044	Aspergillus niger

15	87.2	8.9	8.94	18	AAT765544
14	92.4	9.4	2054	17	AAO210465
43	95	9.7	801	22	AAO240565
41	95.6	9.7	2074	AAO00977	AAI166000
42					
40	96.2	9.8	847	21	AAAO72454
39	96.8	9.7	847	21	AAAO72454
38	97.6	9.9	954	18	AAT610238
37	98.2	10.0	685	13	AAO422385
36	99.8	10.2	2059	14	AAO426888
35	101.4	10.3	2967	17	AAO426888
34	103	10.5	1927	22	AAO426888
33	105.4	10.7	904	18	AAT648844
32	108.8	11.1	1207	17	AAT642374
31	119	12.1	747	19	AAO423074
30	119.2	12.1	558	19	AAO423074
29	124	12.6	2898	21	AAO424400
28	129.6	13.2	2055	19	AAO424400
27	136.8	13.9	2225	22	AAO424400
26	138	14.0	1174	18	AAT715803
25	142.6	14.5	549	18	AAT60636
24	144.6	14.7	573	19	AAO630988
23	146.4	14.9	556	21	AAO462151
22	149	15.2	1581	15	AAO462151
21	164	16.7	516	13	AAO288288
20	165.2	16.8	927	15	AAO746386
19	168.4	17.1	675	14	AAO365566
18	171.8	17.5	572	14	AAO365566
17	181.8	18.5	1281	18	AAT715803
16	183.4	18.7	1057	11	AAO404308
15	187.8	19.1	1273	16	AAO404308
14	190	19.3	1015	20	AAO404308
13	190	19.3	1015	14	AAO547775
12	194.2	19.8	822	19	AAO547775
11	197.2	20.1	1375	18	AAT649300
10	197.2	20.1	1375	17	AAT649300
9	197.2	20.1	1375	17	AAT649300

ALIGNMENTS

RESULT	1
AAT40742	
ID	AAT40742 standard; cDNA; 983 bp.
XX	
AC	AAT40742;
DI	21-MAY-1997 (first entry)
XX	
DE	xylanase coding sequence.
XX	
KW	Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermascus chromium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Thielavia; Hirsutiella; Papiliomyces; animal feed additive; in vivo breakdown; plant cell wall; growth rate; feed conversion; ss.
OS	Thermomyces lanuginosus.
XX	
FH	Key
FT	Location/Qualifiers
FT	KL..70R
PT	/tag-a
PT	/product- xylanase
XX	
IN	M09623062-A1.
XX	
PD	01-AUG-1996.
XX	
PP	26-JAN-1996; 96WO-DK00046.
XX	
PK	26-JAN-1995; 95DK-0000094.
XX	
EA	(NOVO) NOVO-NORDISK AS.
XX	

[illegible]

RESULT	3
AA13813	
ID	AA13813 standard; DNA; 588 bp.

AC	AA513813;
XX	
DT	18-DEC-2001 (first entry)

DE DNA encoding *Thermomyces lanuginosus* xylanase A.
XX
KM Xylanase A: plant cell wall; baking; cereal; starch production; wood;

XX wood pulp bleaching, bleaching liquor, aldehydoxylan, lignosulfonate, urea, urea-XX
XX Thermomyces lanuginosus.

PN WO200165/11-A1.
XX
XX
PI 13-SEP-2001.
XX

PF	08-MAR-2001; 2001WO-1B00426;
XX	
PR	08-MAR-2000; 2000GH-0005585;
PR	27-JUN-2000; 2000GB-0015751;

XX (PANI-) DANISCO AS,
PA
XX
BT S:Phasco O Sorareen TR.

XX
DK
XX
WPI: 2001-596834/67.

PT or modifying plant cell wall, comprises amino acid modifications such
PT that the polypeptide has altered sensitivity to xylanase inhibitor
XX

XX The invention relates to a variant xylanase polypeptide (1) or its fragment having xylanase activity, comprising one or more amino acid

CC wall or for processing a plant material by contacting the plant cell with

CC or planimaterial with (I) or (II). (I) is useful for modifying plant
CC materials, and in baking, processing cereals, starch production,
CC processing wood and enhancing the bleaching of wood pulp. (I)
CC is useful for altering the viscosity derived from the presence of

CC hemicellulose or arabinoxylan in a solution or system comprising plant
CC cell wall material. (1) is useful for preparing a foodstuff such as
CC bread, pretzels, tortillas, cakes, cookies, biscuits or crackers.
CC The present invention represents the coding sequence of *Thermococcus*

CC	<i>lanquinosus</i> xylanase A as described in the method of the invention.
XX	
SO	Sequence 588 BP; 131 A; 178 C; 168 G; 111 T; 0 other;

Query Match	59.58;	Score 585;	DB 22;	Length 588;
Best Local Similarity	100.00;	Prod. No. 1,90-148;		

[illegible]

PT polypeptide of interest
 XX
 PS Claim 14; Page 38-39; 61pp; English.
 XX
 CC The invention relates to a *Pichia* cell comprising at least one copy of
 CC heterologous nucleotide sequence encoding a polypeptide of interest,
 CC where the codon usage of the sequence has been adjusted to match the
 CC preferred codon usage of *P. methanolicus*. The invention also relates to
 CC a method for producing high yields of heterologous codon optimised
 CC polypeptide in a *Pichia* cell. The *Pichia* cell is useful for producing
 CC a polypeptide of interest, where the polypeptide is encoded by a
 CC nucleotide sequence heterologous to *P. methanolicus*. The present sequence
 CC is the mycogenes lamninosus codon optimised xyylase gene which is the
 CC heterologous DNA used in the invention.
 XX
 SU Sequence 678 bp; 180 A; 89 C; 152 G; 257 T; 0 other;

Query Match	48.08;	Score	474;	DB	22;	Length	678;
Best Local Similarity	72.08;	Prod. No.	2,600-94;				
Matches	488;	Conservative	0;	Mismatches	190;	Indels	0;
						Gaps	0

[illegible]

RESULT
AAG94952

ID	AA094952 standard; DNA: 1123 bp.						
XX							
AC	AA094952:						
XX							
D1	02-DEC-1995 (first entry)						
XX							
DE	<i>Humicola insolens xylanase</i> .						
XX							
KW	<i>Xylanase</i> ; DSM 6995; SS.						
XX							
OS	<i>Humicola insolens</i> .						
XX							
FH	Key		Location/Qualifiers				
EF	GDS		126..806				
ET			/*key = a				
XX							
NN	M09515391-A.						
PD	08-JUN-1995.						
XX							
PF	29-Nov-1994: 94WO-US13613.						
XX							
FR	01-DEC-1993: 93US-0161675.						
XX							
PA	(NOVO) NOVO NORDISK BIOTECH INC.						
XX							
P1	Berka RM, Boomathnan KC, Takagi S, Yoder W;						
DR	WP1: 1995-215271/28.						
OR	P-PsDB: AAR78231.						
XX							
PT	<i>Aspergillus japonicus</i> -type cells expressing heterologous protein - esp.						
FT	fungal enzyme, provide high yields without significant prodn. of protease						
PI	or mycotoxin.						
XX							
PS	Example: Page 39-40; 50pp; English.						
XX							
CX	A strain of E. coli contg. the approx. 1,100 bp xylanase HindIII/XbaI cDNA fragment in pYES is deposited in DSM as DSM 6995. The xylanase cDNA fragment is isolated from one of the clones and sequence of the xylanase gene and protein are given in AA094952 and AAR78231 and the gene is deposited as DSM 6995.						
CC							
SQ	Sequence 1123 BP; 249 A; 442 C; 293 G; 239 T; 0 other:						
	Query Match 24.3% Score 239; DR 16; Length 1123; Best Local Similarity 64.4%; Pred No. 1,10-54; Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2						
OY	B7	CTTCCCGCAGGGATATGCACGCCGAAGTCGAAAAAGCAGCAAGAACACTGTAAATTGACAGG	146				
		I I					
Db	197	ctgcctcgagcaacaatccgaacggccttcaagctcgacagcatgaacctccaaccgaacgaataaa	256				
OY	147	CTGGCAGCATGCGTTATTAATTAATTCCTGGTGAGTAGTAGCGTGGAGCGCACCGTAATAAC	206				
		I I					
Db	257	cfcgacgaacacgtactactactatcgtqgtgctgcgacgagcgaggtcacatttcattaacac	316				
OY	207	CAACCTGCAAGCGCGCATACGAGAATCAGTCGACGCGCAGATGGCGCAATCTGTAAGCTGCG	266				
		I I					
Db	317	caacctcgaaggaagaacgcgtactaatgaatttgaaaatgatctaacaacgccgaatatcttcgaatg	376				
OY	267	AAGAGGDTTGAAGCCGCCGTCATGACCAGCAAGGCATATCATTTGACAATATTTAGTAAGG	326				
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Db	377	ttaagtllttgaataccccga--gaacgcgcgcgaacgaatcaacgaaggcgtactttaaccac	438				
OY	327	AATCGGTAACAGTACTGTCGGTCTACGCGTTGGAGATGCGAATCCGCTGAGTAGATATA	386				
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OY	387	CATCGTCGAGGAATTGGTCAACCATATATCTTCTCCAGGCTTAGGATTAAGTAATCG	446				
		I I					
Db	494	tatcatctgaatcttatcaagcaatlaaaatctccgaacgaaggtctcaatlaaaagatcgaatt	553				

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OY	507	CGACGGCACGCCAAMACTTGACGACCAATACTGGTGGTGGCGVAGCAWAAACGGTACGCAAGG	566	
Db	614	cgaaggacgccgagcatcttcagcaattactgctctatccgaaagaaaagaacgatlccgaag	673	
OY	567	TACGCTCCGAAGAGGACCTGGCATTTGACGCGCTGGAGTGTGGATTGATTGAATGTAACAG	626	
Db	674	cctggctcacacatgcaaacaccatcttaacgcgctggagcagcagcagcagcagcagcagc	748	
OY	627	TGACGCTACCTACCAAGATCGGTGGTCAGCGAAGCGCTACTTCGATAGAGAGTATGTCGAT	686	
Db	741	ccaagactactcctacgagatcgtcgtcccccgaagagcttacccaatgatttggaattccgaat	790	
OY	687	GACCTGT 693		
Db	791	ctatgatt 797		
 RESULT 6 AAQ74098 ID AAQ74098 standard; DNA: 1123 BP. XX AC AAQ74098: XX AT 14-NOV-1995 (first entry) XX DE Humicola xylanase gene. XX KW Xylanase; vector: pAXX40-1-1; Aspergillus foetidus; ss. OS Humicola isolens. XX FH Key Location/Qualifiers FT CDS 126..809 FT /*tag= a XX PN W05515490-A. XX PD 08-JUN-1995. XX PE 29-NOV-1994; 94WD-D813612. XX PK 01-DEC-1993; 94DS-0160591. XX PA (NOVO) NOVO NORRISK BIOTECH INC. PI Herika FM, Boomnathan KC, Takagi S, Yoder W; DK WP1: 1995-215270/28. DR P-PSDB; AAR75421. XX PT Aspergillus foetidus cells expressing heterologous enzyme - Fatic. FI fungal lipase or xylanase, provide high yields without significant PI prodn. of protease or mycotoxin. XX PS Disclosure: Page 35-46; 47pp; English. XX CC A DNA fragment (AAQ74098) encoding H. insolens xylanase (AAR75421) was CC isolated from pYES (DSM 6995) and inserted into pBluc14 (containing the CC TAA promoter and AUG termination) to form pAXX40-1-1. This plasmid CC and pial77 (imputing hygromycin B resistance) were used to transform CC protoplasts of A. foetidus N9953. The xylanase yield was 0.12 g/l. XX SQ Sequence 1123 BP; 249 A; 142 G; 293 G; 239 T; 0 other.				
Query Match	24 %;	Score 239;	DB 16;	Length 1123;
Best Local Similarity	64.4%;	Fred. No. 1.1e-54;		
Matches 191;	Conservative 0;	Mismatches 210;	Indels 6;	Gaps 2;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: April 27, 2002, 18:42:36 : Search time 65.8 seconds
(without alignments)
3669.570 Million cell updates/sec

Title: US-09-115-660-1

Sequence: 1 TCGGCGCGAGCTTTCGAT.....AAAAAAAAAAAAAAAAAAAA 983

Scoring table: IDENTITY_MQC
Gapop 10.0, Gapext 1.0

Searched: 48353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767096

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents,NA:*
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2: /cqn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cqn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cqn2_6/ptodata/1/ina/PCIDS_COMB.seq:*
6: /cqn2_6/ptodata/1/ina/backlist1.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result total printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	983	100.0	983	1	US-08-886-765-1
2	983	100.0	983	4	US-09-115-660-1
3	249	24.3	1123	1	US-08-458-023B-3
4	197.2	20.1	1375	2	US-08-468-812-1
5	197.2	20.1	1375	4	US-08-590-563-1
6	194.2	19.8	822	4	US-09-254-733-8
7	190	19.3	1015	2	US-08-121-436A-1
8	181.8	18.5	1281	4	US-08-768-373-1
9	168.4	17.1	675	1	US-07-744-570B-1
10	165.2	16.8	927	1	US-08-507-431-5
11	165.2	16.8	927	2	US-08-902-655A-5
12	165.2	16.8	927	4	US-09-116-622-5
13	165.2	16.8	927	4	US-09-219-277-5
14	165.2	16.8	927	4	US-09-599-661-5
15	162.4	16.5	489	1	US-08-119-169A-7
16	159	16.2	2219	1	US-08-290-979A-7
17	144.8	14.7	573	1	US-08-709-912-18
18	144.8	14.7	573	2	US-09-047-370-18
19	138	14.0	1174	4	US-08-768-373-3
20	119	12.1	744	4	US-09-189-060B-11
21	108.8	11.1	1207	1	US-08-575-964-2
22	108.8	11.1	1207	2	US-08-963-500-2
23	103.6	10.5	2054	4	US-08-981-729-5
24	98.2	10.0	2059	1	US-08-244-686-1
25	97.6	9.9	954	1	US-08-315-695-15
26	96.2	9.8	234	4	US-09-189-060B-46
27	95.8	9.7	847	4	US-09-260-283-1

28	94	9.6	2055	1	US-07-842-349-1	Sequence 1, Appl 1
29	84.6	8.6	941	2	US-08-121-436A-3	Sequence 3, Appl 1
30	82.6	8.4	642	1	US-08-104-445-2	Sequence 2, Appl 1
31	82.6	8.4	1413	1	US-08-104-445-1	Sequence 1, Appl 1
32	82.2	8.4	579	1	US-08-709-912-19	Sequence 1, Appl 1
33	82.2	8.4	579	2	US-09-047-370-19	Sequence 1, Appl 1
34	81	8.2	572	1	US-08-044-621D-3	Sequence 1, Appl 1
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37	77.2	7.9	234	4	US-09-189-060B-48	Sequence 4, Appl 1
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39	74.2	7.5	744	4	US-09-189-060B-1	Sequence 1, Appl 1
40	74.2	7.5	871	1	US-08-698-978-1	Sequence 1, Appl 1
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42	72.4	7.4	663	4	US-08-470-953A-1	Sequence 1, Appl 1
43	72.4	7.4	663	4	US-08-470-953A-2	Sequence 2, Appl 1
44	72.4	7.4	744	4	US-08-470-953A-4	Sequence 4, Appl 1
45	72.4	7.4	744	4	US-08-470-953A-5	Sequence 5, Appl 1

ALIGNMENTS

```

RESULT 1
US-08-886-765-1
Sequence 1, Application US/08886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hansen, Peter Kamp
APPLICANT: Wagner, Peter
APPLICANT: Mullertz, Anette
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: No. 58175000 No. 5817500disk of No. 5817500th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1-30-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lamberts, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Thermomyces lanuginosus
STRAIN: DSM 4109
FEATURE:
NAME/KEY: CDS
LOCATION: 31..705
US-08-886-765-1

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 Db 241 GAGATGCGGCTAGCTGCTGCTGGAAGGCTGGAACCCGAGCTGAACCTGAACCT 300
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 Db 301 ATGCACTTACAGGCTGCTAGCTGCTGGAAGGCTGGAACCTGCTGGAACCT 400
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 QY 901 TCGGCTGCTAGCTGCTAGCTGCTGGAAGGCTGGAACCTGCTGGAACCT 960
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 Db 961 AAAAAAAAAAAAAAAAAAAAAA 983
 RESULT 3
 ? Sequence 3, Application US/08458023B
 ? GENERAL INFORMATION:
 ? PATENT NO. 5657990
 ? APPLICANT: Herka, Randy M.
 ? APPLICANT: Yoder, Wendy
 ? APPLICANT: Takagi, Shinobu
 ? APPLICANT: Heemathub, Karuppan C.
 ? TITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
 ? NUMBER OF SEQUENCES: 16
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: No. 5667990 No. 5667990disk of No. 5667990th America, Inc.
 ? STREET: 405 Lexington Avenue
 ? CITY: New York
 ? STATE: New York
 ? COUNTRY: USA
 ? ZIP: 10174-6201
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION NUMBER: US/08458023B
 ? FILING DATE: 01-JUN-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Lowrey Dr., Karen A.
 ? REGISTRATION NUMBER: 41,274
 ? REFERENCE/INTEL NUMBER: 4086,010-US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 212-867-0123
 ? TELEFAX: 212-874-9655
 ? INFORMATION FOR SEQ ID NO: 3:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1123 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: DNA (genomic)
 ? HYPOTHETICAL: NO
 ? ANTI-SENSE: NO
 ? FRAGMENT TYPE: Internal
 ? ORIGINAL SOURCE:
 ? ORGANISM: Humicola insolens
 ? INDIVIDUAL ISOLATE: DSM 6995
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 126..806
 ? US-08 458-023B-1
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 Best Local Similarity 64.4%; Pred. No. 1,80-58;
 Matches 391; Conservative 0; Mismatches 210; Indels 6; Gaps 2;
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 Db 197 GCTTCGCGGCTAGCTGCTGCTGGAAGGCTGGAACCTGCTGGAACCT 256
 QY 147 CTTCGCGGCTAGCTGCTGCTGGAAGGCTGGAACCTGCTGGAACCT 206
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 QY 267 AAGGCTGCTGCTAGCTGCTAGCTGCTGGAAGGCTGGAACCTGCTGGAACCT 326
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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/590,563
 FILING DATE: 26-JAN-1996
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/468,812
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/332,412
 FILING DATE: 31-OCT-1994
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/282,001
 FILING DATE: 29-JUL-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Rudalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 1050.0340003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1375 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 303..1334
 US-08-590-563-1

Query Match 20.1% Score 197.2; DB 4; Length 1375;
 Best Local Similarity 58.6%; Pred. No. 1,46-46;
 Matches 403; Conservative 0; Mismatches 273; Indels 12; Gaps 3;
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 635 ACTGAGATGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 994
 Db 937 ACTGAGATGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 996
 695 CCGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
 Db 997 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1024

RESULT 6
 US-09-254-733-8
 Sequence 8, Application US/09254733
 Patent No. 6277596
 GENERAL INFORMATION:
 APPLICANT: MATANABE, MANABU
 APPLICANT: MORIYA, TATSUKI
 APPLICANT: AYOAGI, KAORI
 APPLICANT: SUMIDA, NAOMI
 APPLICANT: MURAKAMI, TAKESHI
 TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS PRODUCTION
 TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
 FILE REFERENCE: 99-0266*/J(C)(M/C)/0014
 CURRENT APPLICATION NUMBER: US/09-254,733
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 822
 TYPE: DNA
 ORGANISM: TRICHODERMA VIRIDE MC300-1
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (14)..(112)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (14)..(112)
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (113)..(809)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (113)..(285)
 FEATURE:
 NAME/KEY: inton
 LOCATION: (286)..(412)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (413)..(809)
 US-09-254-733-8

Query Match 19.8% Score 194.2; DB 4; Length 822;
 Best Local Similarity 69.0%; Pred. No. 86-46;
 Matches 281; Conservative 0; Mismatches 123; Indels 3; Gaps 1;
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 Db 402 CCGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 461
 446 GCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405
 Db 462 TCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 521

ATTORNEY/AGENT INFORMATION:
NAME: Artis, Cheryl T.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.214-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723, 727..849, 853..900, 904..927)
US-08-902 655A-5

Query Match 16.8%; Score 165.2; DB 2; Length 927;
Best Local Similarity 57.9%; Pred. No. 1.4e-47;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;

DB 107 CGAGAGCTGAAAGGACGACAGACACCCCAACTGGAGGGGTGCATGATGATTAAT 166
DB 134 CTGGCTGTGCTGGGCGCTGGCTGGACGCTCCACTGCTACTGAAAGGCTATATATA 193
DB 167 ATTCCTGGTGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 226
DB 194 GCTTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253
DB 227 ACAGAGTACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 286
DB 254 ACAGAGTACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 312
DB 287 TGAAGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 342
DB 313 AGTGTATAGGATTAAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTAT 372
DB 343 CTGGCTGTGCTGGGCGCTGGCTGGACGCTCCACTGCTACTGAAAGGCTATATATA 402
DB 373 CTCTCGCTTACGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 432
DB 403 GGCAGCTATGATGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 462
DB 433 GGGAGATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
DB 463 ATCTATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 522
DB 493 ACATACAAATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 592
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DB 613 AAGCATTTCAATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 669
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DB 670 AATGCTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 729
DB 703 GAGTAAAG 710
DB 740 CTCTGAGA 747

RESULT 12
US-09-115-622-5
Sequence 5, Application US/09116622
Patent No. 6080567

GENERAL INFORMATION:
APPLICANT: Kotof, Lene V.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Christgau, Stephan
APPLICANT: Heid-Hansen, Hans P.
APPLICANT: Dahlborg, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: St. Joan O.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mulleritz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60805670 No. 60805670 disk of No. 60805670h America, Inc.
STREET: 405 Lexington Avenue, 44th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,622
FILING DATE: 16-July-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Artis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..723, 727..849, 853..900, 904..927)
US-09-115-622-5

Query Match 16.8%; Score 165.2; DB 3; Length 927;
Best Local Similarity 57.9%; Pred. No. 1.4e-47;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;

DB 107 CGAGAGCTGAAAGGACGACAGACACCCCAACTGGAGGGGTGCATGATGATTAAT 166
DB 134 CTGGCTGTGCTGGGCGCTGGCTGGACGCTCCACTGCTACTGAAAGGCTATATATA 193
DB 167 ATTCCTGGTGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 226
DB 194 GCTTCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 253
DB 227 ACAGAGTACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 286
DB 254 ACAGAGTACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 312
DB 287 TGAAGGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 342
DB 313 AGTGTATAGGATTAAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTAT 372
DB 343 CTGGCTGTGCTGGGCGCTGGCTGGACGCTCCACTGCTACTGAAAGGCTATATATA 402
DB 373 CTCTCGCTTACGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 432

```

1 TYPE: nucleic acid
2 STRANDEDNESS: single
3 topology: linear
4 MOLECULE TYPE: DNA (genomic)
5 FEATURE:
6 NAME/KEY: CDS
7 LOCATION: join(3)..723..727..849..853..900..904..927)
8 OS-DG: Z19-277-5

Query Match      16.8% Score 165.2; DB:4; Length 927;
Best Local Similarity 47.9%; Prev. No. 1,46-47;
Matches 452; Conserved 0; Mismatches 248; Indels 8; Gaps
QY 107 CAGAGTTCGAAAGAGCAGCAGCAATCCCAATCTGAGAGCGCGCATGCTATTACT 166
DB 114 CTGGCTCTCTCTGGCGCTGGGATGGTAACTTCAGTCTGCTTACGAGCGATTATCTATA 193
QY 167 ATTCTGGTGGAGTACGCTGTGAGAGCGACAGCCGCTGACATGAACTGGAAGCGGAACT 226
DB 194 GCTTCTGGCATATATATATTAAGCGCGCATGTTGAAATATAGTAAACGCTCTGGGCGCTCT 253
QY 227 ACGAATCAAGCTGGGAGAAATGCGGCAAGCTGGCTGGGAGAAAGCGAGTGAATCTCCGCG 286
DB 354 AAGGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 413

```

[illegible]

APPLICANT: Mulleritz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62286300 No. 62286300disk of No. 62286300 America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/599,661
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/116,622
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Agilis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954, 224-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ. ID NO.: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(11..723, 727..849, 853..900, 904..927)
US-09-599-661-5

Query Match 16.8% Score 165.2; DB 4; Length 927;
Best Local Similarity 57.9% Pred. No. 1,4e-47;
Matches 352; Conservative 0; Mismatches 248; Indels 8; Gaps 3;
QY 107 GGGAGCTGGAAAGCGAGACACCGCCGACGCGGAGGCGCTGGATGATGGTATTAAT 156
DB 134 CTGGCTTTCATGGGCGCTGCGAGTGGACCTGCACTGGCTATCGAAAGGCTATTAATA 193
QY 167 ATTCTGGTGGAGTGAAGTGGAGCGAGGCGACGTACAGTAAATGGAAGGCTAACT 226
DB 194 GCTCTGTGAAGCGATGGGCGAGGCGGCGATTTGATACAGCAAGGCGGCGGCTGGCT 253
QY 227 AGGCAATAGCTGGGAGCATGGCGTAACTGTGCGTGGAAAGGCTGGAAATTTGGAGC 286
DB 254 ACACGCTGACCTGCTGATGGGCTGGAACTTCGTGGTGGAAAGGCTGGAAAGCTG 312
QY 287 TGAAGCGAAGCGCATCGACTTGAAGGCTGTTTACGAGC-----AAAGCGTAATGAT 342
DB 413 AGTGTCAATGACATTACTTACTCGAGTCTCTGGACCGACACCAAAATATATATATAT 472
QY 443 CTGCTGGTGAAGTGGAGCGGCGAAGCGCTGGAGTATTAATGTTGGAAAGT 402
DB 473 CTGCTGGTGAAGTGGAGCGGCGAAGCGCTGGAGTATTAATGTTGGAAAGT 432
QY 403 GGCACATATGATCTTCTGCTGCTGGCTAGCAATCTAGGAATTTGGAGTATGAAAT 462
DB 433 GCGAGTATGACCTGGCTGCTGCTGGCTAGCAATCTAGGAATTTGGAGTATGAAAT 492
QY 463 ATGATATGATCTGGAGTATGCTGGCTAGCAATCTAGGAATTTGGAGTATGAAAT 522

DB 493 ACATACATATATTTACGGGCGACCGGACCGACCGGCTGCTCATCTAGGCAAGGCTACT 552
QY 523 TTGACCAATATAGTGGTGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 582
DB 553 TTGACCAATATAGTGGTGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
QY 583 TGGCTATGACGCTGGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 642
DB 613 AACCATTTAATGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
QY 643 ATGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 702
DB 670 ATGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 729
QY 703 GCGTACA 710
DB 730 GCTGACA 737

RESULT 15
US-08-119-169A-7
Sequence 7, Application US/08119169A
Patent No. 5610048
GENERAL INFORMATION:
APPLICANT: Schuelin, Martin
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboe, Henrik
APPLICANT: Halckier, Torben
APPLICANT: Pedersen, Lars S.
TITLE OF INVENTION: XYLANASE, CORRESPONDING RECOMBINANT DNA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56100480 No. 5610048disk of No. 56100481, America
STREET: 405 Lexington Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-4201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,169A
FILING DATE: 21-SEP-1993
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94160027.4
FILING DATE: 02-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE92/00099
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3588, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867 0124
TELEFAX: 212-867-0298
INFORMATION FOR SEQ. ID NO.: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Hamifolia insolens
STRAIN: DSM 1800
US-08-119-169A-7

CY	647	AACATCTTCCAACTCAAGGTCGGCGTGCGTTGGATTGTGAAGAATAAGGCATCATC	TACC
ID	179	TT	TT
CY	648	TACTAATGCTGTGGTAAGGTCAGGACATCTTACTGCCAACAGAGGTATGCAATATCT	GAG
ID	180	TT	TT
AB	181	TACATACATCTGGCGTAGGAGTCTCACAGATACAGGAGGCTCTGGGACCATCATG	GG
RESULT	5		
DEFINITION	BMI44B1Z WHE03452.F11 F11ZS wheat Fusarium graminearum infected spike cDNA library tititium aestivum cDNA clone WHE03452.F11 F11, mRNA	542 bp	Uncon EST_28 NOV 2001
VERSION	BMI44B1Z		
KEYWORDS	BMI44B1Z.1 GI:17142836		
SOURCE	EST.		
ORGANISM	wheat		
REFERENCE	tititium aestivum Eckardt et al Viticulture and Enology; Strophophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; ? Triticeae; Triticeae. 1 (bases 1 to 542) Krieger,W.M., Lazov,G.K., Miller,S.S., Muellerbauer,C.T., Mitter,K., Pratschky,J., Kausch,Fiedler, S., Gaudin,R., Tong,J.C., Vancura,V., and Wilson,D.E. The structure and function of the expressed portion of the wheat genes Fusarium graminearum infected spike cDNA library contact: olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel : 510/595/773 Fax : 510/595/818 Email : anderso@nrc.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20. No effort was taken to identify ESTs of fungal origin from this library. Thus this EST Seq primer: Stratiomone SK primer: forward/reverse primers:		
FEATURES	Source		
ORIGIN	1..542		
	/organism "Triticum aestivum"		
	/cultivar "Sunbelt"		
	/db_xref "taxon:4565"		
	/clone "WHE03452.F11 F11"		
	/cotton_lib "wheat Fusarium graminearum infected spike cDNA library" /tissue_type "spike" /dev_stage "Adult plant" /lab_host "E. coli SOLR" Note Vector: lambda Uni-ZAP XR, excised plasmid phycoscript SK; Site 1: EORI; Site 2: XbaI; Plants were grown in the greenhouse. Spikes were sprayed at anthesis with Fusarium graminearum total RNA, and poly(A) RNA were prepared and pooled from infection at 0, 6, 12, 24, 36 and 48 hours after inoculation. A cDNA library was made and the cDNA clones were in vivo excised to give phycoscript phageids in 0. Murdhauer lab at the University of Minnesota (Krieger, W.M., Muellerbauer, C.T., Pratschy, J., Vance, T.). The cDNA library should contain genes of both wheat and fungal pathogen origin. Plasmid RNA preparation and DNA sequencing were performed in the Olin Anderson Lab (all other authors). "		
PAGE COUNT	114 a	154 e	152 g 155 t
ORIGIN			
Query Match	18.5%	Score 181.6;	Identities 542;
Best Local Similarity	65.1%;	Frac. No. 1,2e+20;	Lenth 542;

[illegible]

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: idean@clemson.edu
Seq primer: TAATACCACTACTATAGGG
Class: BAC ends
High quality sequence start: 42
High quality sequence stop: 117.
Location/Qualifiers

FEATURES

source

1..646
/organism="Maizeprothe arisa"
/strain="70-15"
/db_xref="taxon:148305"
/clone_lib="maxb002H24f"
/clone_lib="CUGL Rice Blast BAC Library"
/tissue_type="protoplasts"
/lab_host="E. coli DH10B"
/note="Vector: pBACWich; Site_1: HindIII; Site_2: HindIII;
Rice blast is one of the most devastating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
numerous aspects of the fungal-host interaction. In
order to facilitate genome wide analysis, a BAC library
containing 9216 clones with an average insert size of 130
kbp was constructed. This library represents greater
than 25X genome coverage. High density colony filters
are available upon request."

BASE COUNT 92 a 240 c 148 g 183 t 4 others
ORIGIN

Query Match 12.4% Score 121; DB 12; Length 646;

Host Local Similarity 61.1%; Pred. No. 1e-10;

Matches 196; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

DB 372 GCTGTCGAGTATTACATCGTCGAGAACCTTGCGACCTATGATCTTCTGCTGCTGCTAC 431

DB 372 GATGATGATGATTTAGGTGGAGAGCTTTGCAAGTTAGTAGTGGATGAGAGAGAA 313

DB 432 CGATGTAGAGCTGCGAGTCGAGAGTAGATGATGATGATGATGATGATGATGATGAT 491

DB 312 CAACGGCGGGCTTCCTCACCCTCGAGAGAGACACTACCAATCTGCAACATGCTGCTA 253

DB 492 CAACGCACTTACATCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551

DB 252 CAACGATGCTGCTGATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 193

DB 552 CAACGAGACATAGTGTGATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611

DB 192 CAACGAG 133

DB 612 TTGAATATTAAGGCTGACACTATGACATGCTGCAAGAGAGAGAGAGAGAGAGAG 671

DB 132 CATTACACTGCTGAG 73

DB 672 GCGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 692

DB 72 GCGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 52

RESULT 14

AM133010

LOCUS AM133010 293 bp mRNA linear EST 30 NOV-2001

DEFINITION Gm-c1014-391 5' similar to SW:EF043811 ESTIMATION FACTOR

ACCESSION G. CHLOROPLAST PRECURSOR ? mRNA sequence.

VERSION AM133010.1 GI:6134617

KEYWORDS EST.

SOURCE soybean.

ORGANISM

Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae;
Glycine.

REFERENCE

1 (bases 1 to 293)

Shoemaker, R., Klein, P., Volkin, L., Eppel, J., Corry, J. V., Khanna, A., Holla, B., Marra, M., Hillier, L., Kueh, L., Martin, J., Beck, J., Wylie, T., Underwood, K., Steptoe, M., Theising, R., Alton, M., Howitt, Y., Person, B., Swaffler, J., Gibbons, M., Papad, B., Harvey, N., Schmit, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Morgan, R., Waterson, R. and Wilson, R.

TITLE

Public Soybean EST Project

JOURNAL

Unpublished (1999)

COMMENT

Contact: Shoemaker R/public Soybean EST project
Public Soybean EST project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: rst@wustl.edu

This clone is available through: Rosden, Introgen Corp. 2180
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800) 543 4363 or contact via email: cory@roden.com

Seq primer: -40bp from 5' end.

FEATURES

source

1..293
/organism="Glycine max"
/db_xref="taxon:3847"
/clone_lib="GENOME SYSTEMS CLONE ID: Gm-c1014-391"
/tissue_type="Whole seedlings, 2-3 week old seedlings;
greenhouse grown"
/lab_host="X110-Gold"
/note="Vector: pBluescript II XE; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from whole seedlings of 2-3 week old greenhouse grown
plants. The cDNA library was prepared using the Stratagene
pLyscript II XE cDNA library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly (dI) sequence with a XhoI restriction
site. Froel adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into X110-Gold host cells. This library
was constructed by Dr. Randy Shoemaker and Dr. John
Eppel."

BASE COUNT 146 a 58 c 44 g 65 t
ORIGIN

Query Match 5.0% Score 48.8; DB 9; Length 293;

Best Local Similarity 65.7%; Pred. No. 96;

Matches 71; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

DB 876 TTTCGCTGATTTCTGCAAAAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 945

DB 115 TTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 174

DB 946 GCATTTAGAGCTTTCAGCTTGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 984

DB 175 ATGATTTGGGCTTTGTTTGTAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 222

RESULT 15

H1492941

LOCUS H1492941 564 bp mRNA linear EST 29 AUG 2001

DEFINITION d13b10.w1 Motion Fetal corneal Hemo saponin cDNA clone

IMAGE:2484844 3' mRNA sequence.

ACCESSION H1492941

VERSION H1492941.1 GI:15332275

KEYWORDS EST.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2002, 17:23:05 ; Search time 117.85 Seconds
(without alignments)
212.063 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1238
Sequence: 1 MWGTPVALAALATGALAF.....VATCEYSSGYARITVADVG 225

Scoring table: HUSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
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6: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
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15: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
16: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
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18: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /net/abss06/SIDSI/qcqdqdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	225	17	AAW01112
2	1238	100.0	225	17	AAW05187
3	1083	87.5	194	21	AAW48543
4	965	77.9	194	21	AAW48542
5	806.5	65.1	221	21	AAW48548
6	688.5	55.6	227	16	AAW78231
7	688.5	55.6	227	16	AAW75421
8	684.5	55.4	223	14	AAW57422
9	684.5	55.3	223	14	AAW47122
10	684.5	55.3	223	20	AAW67567
11	678.5	54.8	261	18	AAW18115

12	663	53.6	197	19	AAW60736
13	663	53.6	197	21	AAW48537
14	663	53.6	197	21	AAW98068
15	662.5	53.5	230	18	AAW18116
16	636.5	51.4	190	19	AAW60741
17	636.5	51.4	190	21	AAW99678
18	635.5	51.3	190	19	AAW60743
19	635.5	51.3	190	21	AAW99680
20	634.5	51.3	190	21	AAW48538
21	632.5	51.1	190	19	AAW60744
22	632.5	51.1	190	21	AAW99681
23	632	51.1	225	21	AAW48545
24	631.5	51.0	190	19	AAW60284
25	631.5	51.0	190	21	AAW99735
26	631	51.0	225	18	AAW4597
27	630.5	50.9	190	21	AAW48539
28	630.5	50.9	190	21	AAW48541
29	629	50.8	225	15	AAW59867
30	628.5	50.8	190	19	AAW60282
31	626.5	50.6	190	21	AAW99736
32	611.5	49.4	217	22	AAW09176
33	610.5	49.3	223	21	AAW58149
34	597.5	48.3	226	19	AAW79082
35	587.5	47.5	335	21	AAW48534
36	586.5	47.4	306	15	AAW63791
37	573	46.3	338	16	AAW73967
38	572	46.2	231	20	AAW44183
39	568	45.9	189	19	AAW60740
40	568	45.9	189	21	AAW99677
41	566	45.7	344	17	AAW24480
42	566	45.7	344	18	AAW23338
43	562.5	45.4	191	19	AAW60737
44	562.5	45.4	191	21	AAW98069
45	554.5	44.8	191	19	AAW60280

ALIGNMENTS

RESULT	1
ID	AAW01112
AAW01112	standard; Protein; 225 AA.
AC	AAW01112;
DT	21-MAY-1997 (first entry)
XX	XX
DE	Xylanase.
XX	XX
KW	Xylanase; Thermomyces lanuginosus strain DSM 4109; Humicola; Thermomycetes;
KW	Chaetomium; Mucor; Talaromyces; Malbranchea; Myceliophthora; Heliomyces;
KW	Pyrenopeziza; Paecilomyces; animal feed additive; in-vivo breakdown;
KW	plant cell wall; growth rate; feed conversion.
XX	XX
OS	Thermomyces lanuginosus.
XX	XX
PN	W09623062-A1.
XX	XX
PD	01-AUG-1996.
XX	XX
PE	26-JAN-1996; 96MD-DK00046.
XX	XX
PR	26-JAN-1995; 95DK-0000094.
XX	XX
PA	(NOVO) NOVO-NORDISK AS.
XX	XX
PI	Hansen PK, Knapp III, Muelleritz A, Wagner P.
DR	WPI: 1996-454790/45.
XX	XX
DR	N-PSDB: AAT40742.
XX	XX
PT	Fungal xylanase precips. for use as animal feed additives - and DNA construct for producing recombinant Thermomyces xylanase

Xylanase A of Schizothraustium communis
S. commune xylanase
Chaetomium thermophilum
Xylanase of Trichoderma
T. harzianum xylanase
Xylanase 11 of Trichoderma
T. reesei xylanase
Trichoderma viride xylanase of Trichoderma
T. viride xylanase
Aspergillus awamori
Modified xylanase
Mutant T. reesei xylanase
Aspergillus niger
Trichoderma harzianum
Tichoderma reesei
Aspergillus tubingensis
Aspergillus nidulans
Modified xylanase
Mutant T. reesei xylanase
Penicillium glaucum
Penicillium funiculosum
Aspergillus tubingensis
Streptomyces lividus
Aspergillus aculeatus
T. fusca xylanase
Streptomyces olivaceus
Xylanase A of Thermomyces
T. fusca xylanase
Actinomyces sp. D
Actinomyces sp. D
Xylanase B of Streptomyces
S. lividans xylanase
Modified xylanase

XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring *Bacillus circulans* xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative
CC to the naturally occurring *B. circulans* xylanase. They may be used as
CC the active compound in a bleaching agent which is used for bleaching
CC pulp.
XX
XX Sequence 194 AA:
SU
Query Match 87.5%; Score 1083; DB 21; Length 194;
Best local Similarity 100.0%; Pred. No. 8, 6e-95;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
YY 33 TTPNSGEMHIGYYSWMSDGAQATYTNLEGGTYEISWEGGNEVGKRMNPGLNAAH 92
DB 2 ttpnsqwhdyyswmsdgaqatynleggtyelswgqgnlvqkxmpnlnarh 61
YY 93 FEVYQPNNSYLAAYGWTRNPLVEYYIVENFGTDPSSGATDAGTVECGSTYRLGKT 152
DB 62 fegvyqpnnsylaaygwtrnplveyyivenfgtdpssgatdgtvecgstyrlgkt 121
YY 153 RVNAPSIDGTFDTQVSWSVQKRTSGTGTGCHPDAMARAGLNVDHYVIVALEGYE 212
DB 122 rvnapsidgtfdtqvwsvqrkrtsgtvtgchpdamaraglnvndhyvivalergyf 181
YY 213 SSGYARITVADVG 225
DB 182 ssgyaritvadvg 194
RESULT 4
AA48542
ID AA48542 standard; Protein: 194 AA.
XX
AC AA48542:
XX
DT 05-MAR-2001 (first entry)
XX
DE *Puccinomyces variotii* xylanase.
XX
KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
KM bleaching agent.
XX
OS *Puccinomyces variotii*.
XX
PN W0200068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000MO-US13172.
XX
PR 12-MAY-1999; 9905-013714.
XX
PA (XENC-) XENCOR INC.
XX
PI Benzien JM.
XX
DR WPI: 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermostability,
PT alkalophilicity or thermostability relative to the naturally occurring
PT *Bacillus circulans* xylanase is used in an agent for bleaching pulp -
XX
PS Disclosure: Fig 16K; 114pp; English.
XX
XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring *Bacillus circulans* xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative
CC to the naturally occurring *B. circulans* xylanase. They may be used as
CC the active compound in a bleaching agent which is used for bleaching
CC pulp.

CC enhanced thermostability, alkalophilicity or thermostability relative
CC to the naturally occurring *B. circulans* xylanase. They may be used as
CC the active compound in a bleaching agent which is used for bleaching
CC pulp.
XX
XX Sequence 194 AA:
SU
Query Match 77.9%; Score 965; DB 21; Length 194;
Best local Similarity 87.6%; Pred. No. 1,4e-83;
Matches 169; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
YY 33 TTPNSGEMHIGYYSWMSDGAQATYTNLEGGTYEISWEGGNEVGKRMNPGLNAAH 92
DB 2 ttpnsqwhdyyswmsdgaqatynleggtyelswgqgnlvqkxmpnlnarh 61
YY 93 FEVYQPNNSYLAAYGWTRNPLVEYYIVENFGTDPSSGATDAGTVECGSTYRLGKT 152
DB 62 fegvyqpnnsylaaygwtrnplveyyivenfgtdpssgatdgtvecgstyrlgkt 121
YY 153 RVNAPSIDGTFDTQVSWSVQKRTSGTGTGCHPDAMARAGLNVDHYVIVALEGYE 212
DB 122 rvnapsidgtfdtqvwsvqrkrtsgtvtgchpdamaraglnvndhyvivalergyf 181
YY 213 SSGYARITVADVG 225
DB 182 ssgyaritvadvg 194
RESULT 5
AA48548
ID AA48548 standard; Protein: 221 AA.
XX
AC AA48548:
XX
DT 05-MAR-2001 (first entry)
XX
DE *Cochliobolus carbonum* xylanase.
XX
KW Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;
KM bleaching agent.
XX
OS *Cochliobolus carbonum*.
XX
PN W0200068396-A2.
XX
PD 16-NOV-2000.
XX
PF 12-MAY-2000; 2000MO-US13172.
XX
PR 12-MAY-1999; 9905-013714.
XX
PA (XENC-) XENCOR INC.
XX
PI Benzien JM.
XX
DR WPI: 2000-679800/66.
XX
PT Non naturally occurring XA protein with enhanced thermostability,
PT alkalophilicity or thermostability relative to the naturally occurring
PT *Bacillus circulans* xylanase is used in an agent for bleaching pulp -
XX
PS Disclosure: Fig 16Q; 114pp; English.
XX
XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring *Bacillus circulans* xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative
CC to the naturally occurring *B. circulans* xylanase. They may be used as
CC the active compound in a bleaching agent which is used for bleaching
CC pulp.

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OM protein - protein search, using SW model

Run on: April 27, 2002, 17:28:46 ; Search time 30.85 seconds
(without alignments)
178.145 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1238

Sequence: 1 MVEFTPVALLAALATGALAF.....VATGYPSSYARITVALWG 225

Scoring table: BIOSUM62
Gap: 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cun2_6/prodata/1/iaa/56_COMB.pep:*
3: /cun2_6/prodata/1/iaa/56_COMB.pep:*
4: /cun2_6/prodata/1/iaa/56_COMB.pep:*
5: /cun2_6/prodata/1/iaa/56_COMB.pep:*
6: /cun2_6/prodata/1/iaa/56_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	225	2	US-08-886-765-2
2	1238	100.0	225	4	US-09-115-660-2
3	688.5	55.6	227	1	US-08-458-0238-4
4	685.5	55.4	223	4	US-09-254-733-7
5	684.5	55.3	223	4	US-08-121-436A-2
6	678.5	54.8	197	1	US-08-768-173-2
7	663	53.6	197	1	US-08-044-621D-29
8	663	53.6	197	2	US-08-709-912-9
9	663	53.6	197	2	US-09-047-370-9
10	662.5	53.5	230	4	US-08-768-173-4
11	636.5	51.4	190	1	US-08-044-621D-28
12	636.5	51.4	190	1	US-08-709-912-14
13	636.5	51.4	190	2	US-09-047-370-14
14	635.5	51.3	190	1	US-08-044-621D-26
15	635.5	51.3	190	1	US-08-709-912-16
16	635.5	51.3	190	2	US-09-047-370-16
17	634.5	51.3	190	1	US-08-044-621D-27
18	632.5	51.1	190	1	US-08-709-912-17
19	632.5	51.1	190	2	US-09-047-370-17
20	628	50.7	225	1	US-08-290-979A-8
21	588.5	47.5	226	1	US-08-507-431-6
22	588.5	47.5	226	3	US-09-116-622-6
23	588.5	47.5	226	4	US-09-219-277-6
24	588.5	47.5	226	4	US-09-599-661-6
25	586.5	47.4	241	1	US-08-902-655A-6
26	571.5	45.2	215	1	US-08-044-621D-34
27	568	45.3	189	1	US-08-709-912-13

28	568	45.9	189	2	US-09-047-370-13	Sequence 13, Appl
29	566.5	45.8	206	1	US-08-315-695-19	Sequence 19, Appl
30	566	45.7	344	4	US-08-468-812-2	Sequence 2, Appl
31	566	45.7	344	4	US-08-590-563-2	Sequence 2, Appl
32	562.5	45.4	191	1	US-08-709-912-10	Sequence 10, Appl
33	562.5	45.4	191	2	US-09-047-370-10	Sequence 10, Appl
34	545.5	44.1	189	1	US-08-044-621D-38	Sequence 38, Appl
35	541.5	43.7	189	1	US-08-709-912-12	Sequence 12, Appl
36	541.5	43.7	189	2	US-09-047-370-12	Sequence 12, Appl
37	540	43.6	216	1	US-08-315-695-20	Sequence 20, Appl
38	529.5	42.8	191	1	US-08-044-621D-35	Sequence 35, Appl
39	529.5	42.8	200	1	US-07-744-570B-2	Sequence 2, Appl
40	525.5	42.4	191	1	US-08-709-912-11	Sequence 11, Appl
41	525.5	42.4	191	2	US-09-047-370-11	Sequence 11, Appl
42	506.5	40.9	278	3	US-09-260-283-2	Sequence 2, Appl
43	499.5	40.3	211	1	US-08-575-964-1	Sequence 1, Appl
44	499.5	40.3	211	2	US-08-963-500-1	Sequence 1, Appl
45	476	38.4	168	3	US-08-591-685-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-886-765-2
Sequence 2, Application US/0886765
Patent No. 5817500
GENERAL INFORMATION:
APPLICANT: Hanssen, Peter Kamp
APPLICANT: Maffett, Aucte
APPLICANT: Knapp, Inge Helmer
TITLE OF INVENTION: Animal Feed Additives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58175000 No. 58175000disk of No. 5817500th America, Inc.
STREET: 405 Lockington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,765
FILING DATE: 1,001-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4324,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-886-765-2

Query Match 100.0%; Score 1238; DB 2; Length 225;
Best local Similarity 100.0%; Pred. No. 2,9e-110;
Matches 225; Conservative 0; Mismatches 0; Gaps 0;

DB 1 MVEFTPVALLAALATGALAFPPAGNATELEKROTTINSEGMHKKYYSKMSKXNAATYTN 60

[illegible]

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CORRESPONDENCE ADDRESS:
ADDRESSEE: GOWLING, Strathby & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1G8
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 800KB Storage
COMPILER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/GB/94/4,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
AGENCY/AGENT INFORMATION:
NAME: Judy A. Eggatt
REGISTRATION NUMBER: 44,076
REFERENCE/CHECKED NUMBER: GB-86-1796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613 786-0199
TELEX: 613 563-9869
FAX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 197
TYPE: Amino Acid
STRANDNESS: No. 5405769 Relevant
Topology: Linear
MOLECULE TYPE:
DESCRIPTION: protein
HYDROPHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Schizophyllum commune
STRAIN: Schizophyllum commune, Xylodase A
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURES:
PUBLICATION INFORMATION:
AUTHORS: Oki T., Yaguchi M., Paice M., & Jurasek
AUTHORS: L.
TITLE:
JOURNAL: Canadian Pod. Biol. Soc. Annu. Meet.
VOLUME:
ISSUE:
PAGES: Abstract 676
DATE: 1988
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-29
Query Match 54.6% Score 663 DB 1 Length 197
Best Local Similarity 61.4% Prod. No. 1,26--55
Matches 119 Conserved 26 Mismatches 43 Indels 6 Gaps 27
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? TELEFAX: 613-563-9869
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? TELEX:
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? INFORMATION FOR SEQ ID NO: 28:
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? SEQUENCE CHARACTERISTICS:
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? LENGTH: 190
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? TYPE: Amino Acid
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? STRANDEDNESS: NO
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? TOPOLOGY: linear
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? MOLECULE TYPE:
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? DESCRIPTION: protein
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? HYPOTHEICAL: NO
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? ANTI-SENSE: NO
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? ORGANISM: Trichoderma harzianum
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? STRAIN: Trichoderma harzianum, 20KD
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? IMMEDIATE SOURCE:
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? POSITION IN GENOME:
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? FEATURE:
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? PUBLICATION INFORMATION:
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? AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
?
? AUTHORS: F., Tan L.U., Senior D.J., & Sadtler
?
? AUTHORS: J.N.
?
? TITLE:
?
? JOURNAL: Xylans and Xylanases
?
? VOLUME:
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? ISSUE:
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? PAGES: 435-438
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? DATE: 1992
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? DOCUMENT NUMBER:
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? FILING DATE:
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? PUBLICATION DATE:
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? RELEVANT RESIDUES IN SEQ ID NO:
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US-08-044-621D-28

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Best Local Similarity 60.7%; Pred. No. 3.7e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 32 OTTPSECHMDEYVYVSWSDGGAQATYTNLEGGTYEISWGDGNTVGGKGNPQINAHAI 91
DB 1 OTIGPTGYSNYYVSWMDGHAGVYTNNGGGSFTVMNSNGNFGKGMQJTKNKVI 60
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QY 92 HFEQVYQNGNSYLAAYVGMTRNPLVEVYIVENFGTYDPSNSGATDGLCTVECKSTYRKKT 151
DB 61 NFGSYNPNNGNSYLSYCGSRNPLLEYIVENFGTYNPGTGATKLGVEVTSQSVVDIYRT 120
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QY 152 TRVNAPSIIIGIQTFQYVSVRPGJKRTSGTVQJGHPDAMARAGLNVNTHHYVQIVATGAY 211
DB 121 QVKNOPSIIGIATFYQYVSVRNRHSSGSVNTANIFNMASHGLTL-GRMIOYIVAVEGY 179
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QY 212 FSSGYARITVA 222
DB 180 FSSGSASTIVS 190
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? STATE: New York
?
? COUNTRY: USA
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? ZIP: 10172 0194
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? COMPUTER READABLE FORM:
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? MEDIUM TYPE: floppy disk
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? COMPUTER: IBM PC compatible
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? OPERATING SYSTEM: PC-DOS/MS-DOS
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? SOFTWARE: Patent in Release #1.0, Version #1.30
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? CURRENT APPLICATION DATA:
?
? APPLICATION NUMBER: US/08/709,912
?
? FILING DATE: 09-SEP-1996
?
? CLASSIFICATION: 435
?
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Olssen M., Warren E
?
? REGISTRATION NUMBER: 27290
?
? REFERENCE/DOCKET NUMBER: 1039,2000
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: (212) 758-2400
?
? TELEFAX: (212) 758-2982
?
? INFORMATION FOR SEQ ID NO: 14:
?
? SEQUENCE CHARACTERISTICS:
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? LENGTH: 190 amino acids
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? TYPE: amino acid
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? STRANDEDNESS: single
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? TOPOLOGY: linear
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? MOLECULE TYPE: protein
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? HYPOTHEICAL: NO
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? ANTI-SENSE: NO
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? FRAGMENT TYPE: internal
?
? ORIGINAL SOURCE:
?
? ORGANISM: Trichoderma harzianum
?
? PUBLICATION INFORMATION:
?
? AUTHORS: Yaguchi, M
?
? AUTHORS: Roy, C
?
? AUTHORS: Watson, D. C.
?
? AUTHORS: Rollin, F
?
? AUTHORS: Tan, L. U. L.
?
? AUTHORS: Senior, D. J.
?
? AUTHORS: Sadtler, J. N.
?
? JOURNAL: Xylan and Xylanase
?
? PAGES: 435-438
?
? DATE: 1992
?
US-08-709-912-14

Query Match          51.4%; Score 636.5; DB 1: Length 190;
Best Local Similarity 60.7%; Pred. No. 3.7e-53;
Matches 116; Conservative 27; Mismatches 47; Indels 1; Gaps 1;

QY 32 OTTPSECHMDEYVYVSWSDGGAQATYTNLEGGTYEISWGDGNTVGGKGNPQINAHAI 91
DB 1 OTIGPTGYSNYYVSWMDGHAGVYTNNGGGSFTVMNSNGNFGKGMQJTKNKVI 60
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QY 92 HFEQVYQNGNSYLAAYVGMTRNPLVEVYIVENFGTYDPSNSGATDGLCTVECKSTYRKKT 151
DB 61 NFGSYNPNNGNSYLSYCGSRNPLLEYIVENFGTYNPGTGATKLGVEVTSQSVVDIYRT 120
?
QY 152 TRVNAPSIIIGIQTFQYVSVRPGJKRTSGTVQJGHPDAMARAGLNVNTHHYVQIVATGAY 211
DB 121 QVKNOPSIIGIATFYQYVSVRNRHSSGSVNTANIFNMASHGLTL-GRMIOYIVAVEGY 179
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QY 212 FSSGYARITVA 222
DB 180 FSSGSASTIVS 190
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RESULT 12
US-08-709-912-14
? Sequence 14, Application US/08709912
? Patent No. 5759840
?
? GENERAL INFORMATION:
?
? APPLICANT: Sung Dr., Wing L.
?
? APPLICANT: Yaguchi Dr., Makoto
?
? APPLICANT: Ishikawa Dr., Kazuhiko
?
? TITLE OF INVENTION: Modification of Xylanase to improve
?
? TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
?
? NUMBER OF SEQUENCES: 54
?
? CORRESPONDENCE ADDRESS:
?
? ADDRESS: Fitzpatrick, Celia, Harper, and Scinto
?
? STREET: 277 Park Ave.
?
? CITY: New York
?

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RESULT 13
US-09-047-370-14
? Sequence 14, Application US/09047370
? Patent No. 5866408
?
? GENERAL INFORMATION:
?
? APPLICANT: Sung Dr., Wing L.
?
? APPLICANT: Yaguchi Dr., Makoto
?

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APPLICATION: SHUKAWA BY G. KAZUHIKO
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: F11patent, Co., Ltd., Barpet, and Seito
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 Z11: 101/2-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPILER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/047,170
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/7709,912
 FILING DATE: 09 SEP 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: OLSON M., WATSON E.
 REGISTRATION NUMBER: 27290
 REFERENCE/PRIOR NUMBER: 1039, 2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2402
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 HYDROPHILIC: No
 ANTI SENSE: No
 FRAGMENT TYPE: Internal
 ORIGINAL SOURCE:
 ORGANISM: Thermobifida barophilum
 PUBLICATON INFORMATION:
 AUTHOR: Yonechi, M.
 AUTHOR: Key, G.
 AUTHOR: Watson, D. G.
 AUTHOR: Bollitt, P.
 AUTHOR: Lau, L. H. L.
 AUTHOR: Sontori, D. J.
 AUTHOR: Stoddert, J. N.
 JOURNAL: Xylan and Xylanase
 PAGES: 435-438
 DATE: 1992

[illegible]

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 511
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 513
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 515
 516
 517
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 519

FILED DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-26

Query Match 51.38; Score 635.5; DB 1; Length 190;
 Best Local Similarity 60.28; Pred. No. 4.6e-53;
 Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 32 QTTNSECWHDGYYYSWMSDGAQATYTNLEGGTYELISWGDGNTLVGKGMNPLNARAI 91
 11
 DB 1 OTTPTGTYNNQYFYYSWMDGAGVTTNCGTQPSYVMSNSGTFVGGKGMWYTKMKVI 60
 QY 92 HFEQVYQPNNSYLAAYGWTNPLVEVYIVENPGTYPPSSGATDICTVCTGNSYTRAKT 151
 11
 DB 61 NFSGVNPNNSYLAAYGWSKRNPLIEVYIVENPGTYNPGATKLEFVTSDSVYDIYRI 120
 QY 152 TRVAPSTIDGTFDQYWSYKDKRTSGTQVTCGHPAMAKAGIANNMGIHYQIVALEHY 211
 11
 DB 121 QRVNOPSITGATFYQYWSVRNRHSSSVANTNHNMAQOGLTL-GTMDYQIVAVEHY 179
 QY 212 FSSGYARITVA 222
 1111 1111
 DB 180 FSSGSASITVS 190

RESULT 15
 US-08-709-912-16
 Sequence 16, Application US/08709912
 Patent No. 5759840

GENERAL INFORMATION:
 APPLICANT: Sana Dr., Wing L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,912
 FILING DATE: 09 SEP-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: O'Shea M., Warren E
 REGISTRATION NUMBER: 27290
 REFERENCE/MARKET NUMBER: 1039, 2000
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 ORIGINAL SOURCE:

ORGANISM: Trichoderma reesei
 STRAIN: xyn 11
 PUBLICATION INFORMATION:
 AUTHORS: Tortorene, A
 AUTHORS: Mach, R. L.
 AUTHORS: Messner, R
 AUTHORS: Gonzalez, R
 AUTHORS: Kalkkinen, N
 AUTHORS: Hakki, A
 AUTHORS: Kudrick, C. P.
 JOURNAL: Biotechnology
 VOLUME: 10
 PAGES: 1461-1465
 DATE: 1992
 US-08-709-912-16

Query Match 51.38; Score 635.5; DB 1; Length 190;
 Best Local Similarity 60.28; Pred. No. 4.6e-53;
 Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 32 QTTNSECWHDGYYYSWMSDGAQATYTNLEGGTYELISWGDGNTLVGKGMNPLNARAI 91
 11
 DB 1 OTTPTGTYNNQYFYYSWMDGAGVTTNCGTQPSYVMSNSGTFVGGKGMWYTKMKVI 60
 QY 92 HFEQVYQPNNSYLAAYGWTNPLVEVYIVENPGTYPPSSGATDICTVCTGNSYTRAKT 151
 11
 DB 61 NFSGVNPNNSYLAAYGWSKRNPLIEVYIVENPGTYNPGATKLEFVTSDSVYDIYRI 120
 QY 152 TRVAPSTIDGTFDQYWSYKDKRTSGTQVTCGHPAMAKAGIANNMGIHYQIVALEHY 211
 11
 DB 121 QRVNOPSITGATFYQYWSVRNRHSSSVANTNHNMAQOGLTL-GTMDYQIVAVEHY 179
 QY 212 FSSGYARITVA 222
 1111 1111
 DB 180 FSSGSASITVS 190

Search completed: April 27, 2002, 18:36:26
 Job time: 4060 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 27, 2002, 18:33:56 ; Search time 52.22 Seconds

(without alignments)
414.020 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1238

Sequence: 1 MGFTPVVALAALATGALAF.....VAIEGYPSSGYARIIIVAWG 225

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 28138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	691.5	55.9	219	2 S71472	endo-1,4-beta-xyla
2	689.5	55.7	227	2 S43919	endo-1,4-beta-xyla
3	689	55.7	241	2 S71473	endo-1,4-beta-xyla
4	684.5	55.3	223	2 S39883	endo-1,4-beta-xyla
5	680.5	55.0	225	1 S57477	endo-1,4-beta-xyla
6	667	53.9	222	2 S39154	xylanase 1 - funu
7	663	53.6	197	1 A44597	endo-1,4-beta-xyla
8	659	53.2	232	2 J07577	endo-1,4-beta-xyla
9	637.5	51.5	221	1 S57469	endo-1,4-beta-xyla
10	636.5	51.4	190	1 A44593	endo-1,4-beta-xyla
11	636.5	51.4	190	1 A44595	endo-1,4-beta-xyla
12	634.5	51.3	190	1 A44594	endo-1,4-beta-xyla
13	595.5	48.4	221	2 J07107	endo-1,4-beta-xyla
14	585.5	47.3	335	2 T50601	endo-1,4-beta-xyla
15	573	46.3	333	1 J05050	endo-1,4-beta-xyla
16	564.5	44.8	241	2 T37005	endo-1,4-beta-xyla
17	553	44.7	240	1 S47512	endo-1,4-beta-xyla
18	549	43.6	240	1 J05091	endo-1,4-beta-xyla
19	529	42.7	644	1 T40712	endo-1,4-beta-xyla
20	528	42.6	661	1 S59613	endo-1,4-beta-xyla
21	505.5	40.8	210	2 C83762	endo-1,4-beta-xyla
22	498	40.2	656	1 S59631	endo-1,4-beta-xyla
23	470.5	38.0	213	1 S40569	endo-1,4-beta-xyla
24	469.5	37.9	213	1 S48126	endo-1,4-beta-xyla
25	468.5	37.8	213	1 S01734	endo-1,4-beta-xyla
26	452	36.5	354	1 S51779	endo-1,4-beta-xyla
27	427	34.5	511	1 J01935	endo-1,4-beta-xyla
28	400	32.3	261	1 S12745	endo-1,4-beta-xyla
29	397.5	32.1	228	1 WMBXBP	endo-1,4-beta-xyla

30	390	31.5	211	2 S46542	endo-1,4-beta-xyla
31	389.5	31.5	789	2 S58235	endo-1,4-beta-xyla
32	388	31.3	211	1 J01198	endo-1,4-beta-xyla
33	385	31.1	211	1 S48229	endo-1,4-beta-xyla
34	372	30.0	229	2 S39155	xylanase 2 - funu
35	371	30.0	954	1 S20907	endo-1,4-beta-xyla
36	365	29.5	781	2 S51592	Xyln precursor - R
37	356	28.8	209	2 J04909	endo-1,4-beta-xyla
38	355.5	28.7	802	2 A36910	xylanase, beta(1,3
39	299.5	24.2	607	2 S49528	endo-xylanase - fun
40	296	23.9	607	2 S24754	endo-1,4-beta-xyla
41	248	20.0	608	2 B54295	xylanase (EC 3.2.1
42	240.5	19.4	266	1 S48865	endo-1,4-beta-xyla
43	145	11.7	50	2 A61149	endo-1,4-beta-xyla
44	115	9.3	2817	2 B97033	uncharacterized pr
45	113	9.1	40	2 P00202	endo-1,4-beta-xyla

ALIGNMENTS

RESULT 1
S71472
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
N:Alternate names: xylanase A
C:Species: Chaetomium gracile
C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A>Title: Two family G xylanase genes from Chaetomium gracile and their expression in
A:Reference number: S71472; M01D:96118924
A:Accession: S71472
A:Molecule type: DNA
A:Residues: 1-219 <YOS>
A:Cross-references: EMBL:D49850; NID:q1339857; P1DN:HA08645.1; P1D:q1339858
A:Accession: S78206
A:Molecule type: protein
A:Residues: 31-45;82-94;152-160 <YOH>
C:Genetics:
A:Introns: 81/2
C:Function: 81/2
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F:42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F:115,206/Active site: Glu #status predicted

Query Match 55.9%; Score 691.5; DB 2; Length 219;
Best local Similarity 59.1%; Pred. No. 1.2e+47;
Matches 133; Conservative 29; Mismatches 54; Indels 9; Gaps 5;

QY	1	MGFTPVVALAALATGALAFPAAGNAT---ELEKROTPPSNGHNGVYSSWMSGAGQAT	57
DB	1	MVSEKAL---LLAGAGALAEFF NVTQNMELVARAGTSGTGNGGPFYFWTQGIYVA	56
QY	58	YTNLEGTVELESMGDDGNNMGCKGWNPGINARMIHFGSYQPPGNSNYIAYNEGTNPPIVE	117
DB	57	YONGAGSYSVQWQNCNPFQGGKGNPGCA-ARTINPSGTFSPGNGSLAYGMPNPVHE	115
QY	118	YVIVFNQGTDPSSGADATVEEDGSIYRIKRTTNAPSLHCTQFQYQWVSHQDKRT	177
DB	116	YVIVESGTYDPSQASKFCTIOODGSIYTIKATTRNOPSIGSTFPIQFWSVKQNHNS	175
QY	178	SGIVQTCGHPDAMARAGLVNGBHYQIVATEGYPSSGYARITVA	222
DB	176	SGSVNVAHNNAMAQGLKLGSHNVOIVATEGYSGSSGSSITVS	219

RESULT 2

S43919
 endo-1,4-beta-xylanase (EC 3.2.1.8) precursor importokunopus (humicola insolens)
 cy:Species: Humicola insolens
 cy:Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 22-Jun-1999
 cy:Accession: S43919
 R:Fullname: H. Holst-Banson, H.P.
 Moll: 499, 1990, 243, 253-260, 1994
 A:Title: A novel method for efficient expression cloning of fungal enzyme genes.
 A:Feature: number: S43919; MIMD:94247864
 A:Accession: S43919
 A:Molecule: type: mRNA
 A:Postdoc: 1, 2, 7 - DAL
 A:Cross_references: EMBL: X76047; NID:q505260; PIDD:OAA5362.1; P1D:q505261
 A:Method: test
 A:Gene: XY1
 cy:Function:
 A:Pathway: xylan degradation
 cy:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 cy:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1/9/Main: signal sequence #status predicted -S105
 F:20/22/Product: endo-1,4-beta-xylanase #status predicted -CMAT
 F:48-225/Domain: endo-1,4-beta-xylanase homology -XY1
 F:112-157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
 F:121,212/Active site: Glu #status predicted

Query	Match	Similarity	Score	Pos. 2	Length
Post Local	Similarity	Pos. 1	Pos. 2	Pos. 3	Pos. 4
Match	Score	Pos. 1	Pos. 2	Pos. 3	Pos. 4
1	1	1	1	1	1
2	2	2	2	2	2
3	3	3	3	3	3
4	4	4	4	4	4
5	5	5	5	5	5
6	6	6	6	6	6
7	7	7	7	7	7
8	8	8	8	8	8
9	9	9	9	9	9
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66	66	66	66	66	66
67	67	67	67	67	67
68	68	68	68	68	68
69	69	69	69	69	69
70	70	70	70	70	70
71	71	71	71	71	71
72	72	72	72	72	72

RESULT 4
 S71474
 c:endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - chaetomium gracile
 c:Spore: chaetomium gracile
 c:date: 09 Dec 1997 #sequence revision 09-Dec-1997 #taxi_change 20 Jun 2000
 c:Accession: S71474; S78207
 c:Yoshino, S.; Ohashi, M.; MoriYama, R.; Kato, M.; Tsukagoshi, N.
 c:J. Genet. 206, 73-80, 1995
 c:Title: Two family G xylanase genes from chaetomium gracile and their expression in *Asp*
 c:reference number: S71472; MIMD:96118924
 A:Accession: S71474
 A:Molecule type: DNA
 A:Restriction: 1,241 - YOS
 A:Accession: F0140965; JMW: D49851; NID:q1349859; PIDN:BA000500.1; PID:q1349860
 A:Accession: S78207
 A:Molecule type: protein
 A:Restriction: 48-44;89-91;153-161 - YOH
 c:domains:
 A:domain: 88/2
 c:Feature:
 A:pairway: xylan-degradation
 c:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 c:Keywords: glycosidase; hydrolase; polysaccharide degradation
 E:140/aminic signal sequence #status predicted - SIF
 E:41-220/Trpduct: endo-1,4-beta-xylanase B #status predicted - MAT
 E:43-220/Trpduct: endo-1,4-beta-xylanase homology - XYL

[illegible]

```

RESULT 4
S19883
endol-1,4-beta-xylanase (EC 3.2.1.8) 11 precursor          tuoucs (Trichoderma reesei)
N:Alternative names: endoxylanase 11
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
A:Accession: S19883; S59884
R:Stablechain, R.: Polakidou, M.; Fagerstrom, R.; Stenlund, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A>Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxy-
A:Reference number: S19883; M0119:940884A2
A:Accession: S19884
A:Molecule type: DNA
A:Residues: 1-223 -SMA-
A:Cross-references: EMBL:S67487; NID:9455906; PIDD:AAH9346.1; PIDD:9455907
A:Experimental source: strain C66a
A:Accession: S59884
A:Molecule type: protein
A:Residues: 44-4349-67; 121 151;178 191 -SAP-
C:Interacts:
A:Gene: xln2
A:Intron: 91/2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo 1,4 beta xylanase; endo 1,4 beta-xylanase homology
C:Keywords: glycoprotein; glycosylase; hydrolysis; polysaccharide degradation
F:1-19/xmain: signal sequence #status predicted -S10-
F:20-33/xmain: propripide #status predicted -PRO-
F:34-223/product: endo 1,4 beta-xylanase 11 #status experimental -MAF-
F:45-223/xmain: endo-1,4-beta-xylanase homology xYL-
F:71-94/Binding site: carbohydrate (ASN) (covalent) #status predicted
F:110-121/Binding site: substrate (TYR) #status predicted
F:119-210/Active site: Glu #status predicted

```

Object	Match	55, 48	Scores	684, 57	DJ	2	Length	2,245	
Host	Local	Similarity	57, 1%	Pred.	No.	4, 50-47			
Matches	128	Conservation	42	MisMatches	61	Totals	4	Gaps	2
OY	1	MYGTFVVALAAALATATLAFPACTNATLELRKQTPENSEMHDDGYYSWMSNRGNADATY	98						
Ob	1	MYSTFSLLAGVAVALSGVLAAAPAEVEHVSNAVEKRQTGPRTGQTNNTPTFSYMNMGAGTGVY	60						
OY	59	FMLDFTTEFLSMGDGNNLVGRMRMNGINARALHEEGYYQPMGNSYLAVYCNMTNPITVEY	118						
Ob	61	TNRGTGGPSSVMSSNSQNFVGTRKGWDLGTRKNRVINFGSNYPNGNSVLSEYCSMDRNLLEY	120						
OY	139	VYVENHGTYEIDHSNGATDTATVTETDNIVRLDATTVNALSLLGLQTFPLQTSVRQURKRN	178						

Mon Apr 29 08:54:05 2002

us-09-115-660-2.rpt

Page 7

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OM protein - protein search, using sw model

Run on: April 27, 2002, 18:36:31 ; Search time 31.77 seconds

(without alignments)
274,218 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 1238

Sequence: 1 MGFPTVMAIAAATGALAF.....VATECYSSGVAKIIVALWG 225

Scoring table: BIOSUM62

Search: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Result No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1248	100.0	225	1 XYN_A_THELA	043097 thermomyces
2	806.5	65.1	221	1 XYN1_COCOA	006562 cochlidiobol
3	689.5	55.7	227	1 XYN1_HUMIN	P55344 humicola in
4	680.5	55.0	225	1 XYN1_EMENT	P55342 emeticella
5	667	53.9	222	1 XYN2_TRIRE	P36217 trichoderma
6	663	53.6	197	1 XYN2_SCHCO	P35809 schizopyll
7	660	53.3	233	1 XYN2_MAGGR	P55345 magnaporthe
8	637.5	51.5	221	1 XYN2_EMENT	P55343 emeticella
9	632	51.1	225	1 XYN2_ASPAK	P48824 aspergillus
10	631	51.0	225	1 XYN2_ASPNG	P55340 aspergillus
11	630.5	50.9	190	1 XYN1_TRIHA	P48793 trichoderma
12	587.5	47.5	335	1 XYNB_STRL1	P26575 streptomyce
13	540	43.6	240	1 XYNB_STRL1	P26220 streptomyce
14	529	42.7	644	1 XYNB_CELFI	P54865 cellulomonas
15	473	38.2	210	1 XYNB_BACST	P45705 bacillus st
16	470.5	38.0	213	1 XYNB_BACST	P18429 bacillus su
17	468.5	37.8	214	1 XYNB_BACST	P09850 bacillus ci
18	427	34.5	512	1 XYNB_CLOS	P34558 clostridium
19	409	32.3	261	1 XYNB_CLOS	P17137 clostridium
20	396.5	32.0	228	1 XYNB_BACPU	P06634 bacillus pu
21	390	31.5	211	1 XYN1_ASPFU	P55331 aspergillus
22	388	31.3	211	1 XYN1_ASPAK	P43557 aspergillus
23	387	31.1	211	1 XYN1_ASPNG	P55342 aspergillus
24	385	31.1	229	1 XYN1_ASPAK	P55342 aspergillus
25	372	30.0	229	1 XYN1_ASPAK	P55342 aspergillus
26	371	30.0	954	1 XYNB_KIMEL	P29126 rumiinosoru
27	355.5	28.7	802	1 XYNB_KIMEL	P29126 rumiinosoru
28	296	23.9	607	1 XYNB_KIMEL	P29127 neocallimas
29	251.5	20.3	625	1 XYNB_KIMEL	P29127 neocallimas
30	248	20.0	608	1 XYNB_KIMEL	P29127 neocallimas
31	106	8.6	772	1 VPA_KOTHA	P35811 fibrobacter
32	104.5	8.4	398	1 CARA_KHINI	P35407 bovine tota
33	102.5	8.3	1286	1 ALDA_PCOL1	P03700 rhizopus ut

RESULT	1	ALIGNMENTS
ID	XYNA_THELA	STANDARD; PRT; 225 AA.
AC	043097:	
DT	15-DEC-1998 (Rel. 37, created)	
DT	15-DEC-1998 (Rel. 37, last sequence update)	
DT	15-JUL-1999 (Rel. 38, last annotation update)	
DE	Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanhydrolase).	
DE	XYNA.	
GN	XYNA.	
OS	Thermomyces lanuginosus (Humicola lanuginosa).	
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.	
OX	NCBI_TaxID=5541;	
RN	(1)	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=DSM 5826 / TSUKLINSKY;	
RX	MEDLINE=97033440; PubMed=8479171;	
RA	Schlaecher A., Holzmann K., Hayn M., Steiner W., Schwab H.;	
RT	Cloning and characterization of the gene for the thermostable	
RT	xylanase Xyna from Thermomyces lanuginosus.*;	
RL	J. Biotechnol. 49:211-218(1996).	
RL	[2]	
RP	X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).	
RC	STRAIN=DSM 5826 / TSUKLINSKY;	
RX	MEDLINE=98426042; PubMed=9753433;	
RA	Gruber K., Klotzsch G., Hayn M., Schlaecher A., Steiner W.,	
RT	Kratky C.;	
RT	*Thermophilic xylanase from Thermomyces lanuginosus: high-resolution	
RT	X-ray structure and modeling studies.*;	
RL	Biochemistry 37:13475-13485(1998).	
CC	-1- FUNCTION: THERMOSTABLE XYLANASE.	
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic	
CC	linkages in xyans.	
CC	-1- PATHWAY: XLAN DEGRADATION.	
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL	
CC	HYDROLASES).	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation	
CC	at the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announc/	
CC	or send an email to license@sib-sib.ch).	
CC	EMBL: 035436; AAB94633.1; -	
DR	PDB: 1YNA; 12-PEH-97.	
DR	InterPro: IPR001147; Glyco_hydro_11.	
DR	Pfam: PF00457; Glyco_hydro_11; 1.	
DR	PRINTS: PR00911; GLYHYDRLASE11.	
DR	PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.	
DR	PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.	
KW	Xylan degradation; Glycolase; Glycosidase; Signal; 3D-structure.	
FT	SIGNAL	1 31
FT	CHAIN	32 225
FT	ACT_SITE	117 117
FT	NOTEDPHILE.	

FT ACT SITE 209 209 PROTEIN DOMAIN
 FT 600 RES 42 42 HYPERLIPIDINE CATABOLIC ACTIVITY
 FT 1301 ETD 141 145
 SQ SEQUENCE 225 AA: 24355 MW: 54479.914566766 CRC64:
 Query Match 100.0% Score 1248; 1461; Length 225;
 Best Local Similarity 100.0%; Ident. No. 1,248-94;
 Matches 225; Conserved 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVEETVALAALAAATGALAPAGNATLEKROTKNSRHHHGYYSWSSKAGATYIN 60
 1 MVEETVALAALAAATGALAPAGNATLEKROTKNSRHHHGYYSWSSKAGATYIN 60
 1 MVEETVALAALAAATGALAPAGNATLEKROTKNSRHHHGYYSWSSKAGATYIN 60
 QY 61 LEEGETVSMGRKGNVWAKGMNGLNAPALHEFEVYQFNNSYLAAYGWMTRNLEVEY 120
 1 LEEGETVSMGRKGNVWAKGMNGLNAPALHEFEVYQFNNSYLAAYGWMTRNLEVEY 120
 1 LEEGETVSMGRKGNVWAKGMNGLNAPALHEFEVYQFNNSYLAAYGWMTRNLEVEY 120
 QY 121 VENEETVDSSTADTGVETKSTVYKAKTRVNAFSDTQTFDQYWSVKDKRST 180
 1 VENEETVDSSTADTGVETKSTVYKAKTRVNAFSDTQTFDQYWSVKDKRST 180
 1 VENEETVDSSTADTGVETKSTVYKAKTRVNAFSDTQTFDQYWSVKDKRST 180
 QY 181 VQTEHPFAMAKGLNVNMDHYGVATFEVSSYKATLVAVG 225
 1 VQTEHPFAMAKGLNVNMDHYGVATFEVSSYKATLVAVG 225
 1 VQTEHPFAMAKGLNVNMDHYGVATFEVSSYKATLVAVG 225
 RESULT 2
 XYN1_CACCA STANBARD PRT: 221 AA
 AC 506562;
 DT 01 FEB 1996 (rel. 41, created)
 DT 01 FEB 1996 (rel. 41, last sequence update)
 DT 15-JUL-1999 (rel. 48, last annotation update)
 DE Endo 1,4-beta-xylanase 1 precursor (E.C. 3.2.1.8) (Xylanase 1)
 DE (1,4-beta-D-xylan xylanohydrolase 1).
 GN XYL1.
 OS Geobacillus carbonum (Bipolaris zeicola).
 OC Eukaryota; Fungi; Ascomycota; Dothideomycetes; Dothiorales;
 OC Pleosporales; Pleosporaceae; Geobacillus.
 OX NCBI_TaxID:5017;
 RN 111
 RP SEQUENCE FROM N.A.
 RP STRAIN NAME 1 / ISOLATE SH111;
 RX MEDLINE 94091417; PubMed 8400476;
 RA Apol P.C.; Pabst J.C.; Holden P.R.; Walton J.D.;
 RT Cloning and targeted gene disruption of XYL1, a beta 1,4 xylanase
 RT gene from the maize pathogen Geobacillus carbonum.*;
 RL Mol. Plant Microbe Interact. 6:467-473(1993).
 BN 121
 RP PARTIAL SEQUENCE.
 RA Holden P.R.; Walton J.D.;
 RT Xylanases from the fungal maize pathogen Geobacillus carbonum.*;
 RL Physiol. Mol. Plant Pathol. 40:49-47(1992).
 QY 1 FUNCTION: MAJOR XYLAN DEGRADING ENZYME. CONTRIBUTES TO THE
 HYDROLYSIS OF ARABINOXYLAN. THE MAJOR COMPONENT OF MAIZE CELL
 WALLS.
 QY 1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylanidic
 linkages in xyans.
 QY 1 PATHWAY: XYLAN DEGRADATION.
 QY 1 SUBCELLULAR LOCATION: Secreted.
 QY 1 TISSUE: THE N THERMOPHILUS IS MARKED.
 QY 1 SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 HYDROLASES).
 QY This SWISS-Prot entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).

OR EMDL: L13596; AAA3024.1;
 OR HSSBY: 043097; YNA.
 OR InterPro: IPR001137; Glyco_hydro_11.
 OR Pfam: PF00457; Glyco_hydro_11; 1.
 OR PRINTS: PR00911; G1HYDGLASB1.
 OR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 OR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 OR Xylan degrading form: glycosidase; signal.
 FT SIGNAL 1 40
 FT CHAIN 41 221
 FT ACT_SITE 115 115 ENDO 1,4 BETA XYLANASE 1.
 FT ACT_SITE 206 206 NITROPHILIE (HY SIMILARITY).
 FT ACT_SITE 81 81 PROTON PUMP (HY SIMILARITY).
 FT CONFLICT 107 107 W -> A (1N REF. 2).
 FT CONFLICT 131 131 G -> A (1N REF. 2).
 FT CONFLICT 131 131 S -> W (1N REF. 2).
 SQ SEQUENCE 221 AA: 23728 MW: 59180.984956086 CRC64:
 Query Match 65.1%; Score 806.5; 1461; Length 221;
 Best Local Similarity 67.9%; Ident. No. 2,365-99;
 Matches 150; Conserved 26; Mismatches 42; Indels 4; Gaps 4;
 QY 1 MVEETVALAALAAATGALAPAGNATLEKROTKNSRHHHGYYSWSSKAGATYIN 60
 1 MVEETVALAALAAATGALAPAGNATLEKROTKNSRHHHGYYSWSSKAGATYIN 59
 1 MVEETVALAALAAATGALAPAGNATLEKROTKNSRHHHGYYSWSSKAGATYIN 59
 QY 61 LEEGETVSMGRKGNVWAKGMNGLNAPALHEFEVYQFNNSYLAAYGWMTRNLEVEY 120
 1 LEEGETVSMGRKGNVWAKGMNGLNAPALHEFEVYQFNNSYLAAYGWMTRNLEVEY 118
 60 GARGSVSSWSSKGNVWAKGMNGLNAPALHEFEVYQFNNSYLAAYGWMTRNLEVEY 118
 QY 121 VENEETVDSSTADTGVETKSTVYKAKTRVNAFSDTQTFDQYWSVKDKRST 180
 1 VENEETVDSSTADTGVETKSTVYKAKTRVNAFSDTQTFDQYWSVKDKRST 180
 1 VENEETVDSSTADTGVETKSTVYKAKTRVNAFSDTQTFDQYWSVKDKRST 180
 QY 181 VQTEHPFAMAKGLNVNMDHYGVATFEVSSYKATLVAVG 221
 1 VQTEHPFAMAKGLNVNMDHYGVATFEVSSYKATLVAVG 218
 1 VQTEHPFAMAKGLNVNMDHYGVATFEVSSYKATLVAVG 218
 RESULT 3
 XYN1_HUMAN STANBARD PRT: 227 AA
 AC P55334; Q12625;
 DT 01-OCT-1996 (rel. 34, created)
 DT 01-OCT-1996 (rel. 34, last sequence update)
 DT 01-Nov-1997 (rel. 35, last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (E.C. 3.2.1.8) (Xylanase 1)
 DE (1,4-beta-D-xylan xylanohydrolase 1).
 GN XYL1.
 OS Homo sapiens.
 OC Eukaryota; Fungi; Ascomycota; Mitosporie Ascomycota; Humicola.
 OX NCBI_TaxID:34413;
 RN 111
 RP SEQUENCE FROM N.A.
 RP MEDLINE 94247647; PubMed 8190078;
 RA Dalgaard H.; Hansen H.P.H.;
 RT "A novel method for efficient expression cloning of fungal enzyme
 RT genes".
 RL Mol. Gen. Genet. 243:253-260(1994).
 QY 1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylanidic
 linkages in xyans.
 QY 1 PATHWAY: XYLAN DEGRADATION.
 QY 1 SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 HYDROLASES).
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 or send an email to license@isb-sib.ch).

60 X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 61 STRAIN 1.40.
 62 MEDLINE 96/02263; PubMed 8755744.
 63 HOOKINGTON R., TOOTHMAN A., LALLIER T., ROYINTE L.,
 64 "COVALENT BINDING OF THREE EPOXYALKYL XYLANSIDES TO THE ACTIVE SITE OF
 65 BETA-1,4-XYLANSASE II FROM TRICHOTHOMA REUSII".
 66 Biochemistry 35:10617-10624(1996).
 67 1. CATALYTIC ACTIVITY: Endohydrolasts of 1,4 beta-D-Xylosidase
 68 1. Lookases in xyloans.
 69 1. PATHWAY: XYLAN DEGRADATION.
 70 1. PDB: THE N TERMIINS IS BLOCKED.
 71 1. SIMILARITY: BELONGS TO GELATINASE FAMILY 6 (FAMILY 11 OF GLYCOSYL
 72 HYDROLASES).
 73
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 75 between the Swiss Institute of Bioinformatics and the EMBL out station.
 76 The European Bioinformatics Institute. There are no restrictions on its
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 80 or send an email to license@isb.slb.ch).

[illegible]

Query Match	54.9%	Score 667	DH 1	Length 222
Host Local Similarity	57.1%	Prod. No. 6,70-48		
Matches 128	Conservative	42	Mismatches 60	Indels 4
				Gaps 3

0Y	1	MOGELTVAIALAATGALAFAG	1	NATHEKOTUPNEKHEKYYSWMSWZACAOAY	58
	1	11111111111111111111	1	11111111111111111111	11
Dib	1	MOSETSL	1	LAASPSKASSTBAAPAESVAVERKOTLOKOTOTYNNAYPESYNSWAGHOCAY	59
0Y	59	ENJEGEYFESWOGACATN1WOKRMWPG1NARA1HEPESYUOPMSYLAAYW1MRN1VEY	118		
	1	11111111111111111111	1	11111111111111111111	11
Dib	60	ENJEGESYNSWMSNSG1NEVGRGMOJGPKRKNV1NEPSYNPMSYLSYV1MSKRN1LEY	119		
0Y	119	1V1ENP1GYT1PSSKAT101ATV1E1KSN1YH1K1KTT1VNA1S1101OT1E1Y1W1SV1R1D1K1S	178		
	1	11111111111111111111	1	11111111111111111111	11
Dib	120	1V1ENP1GYT1PSSKAT1E1V1S1K1SV1D1Y1E1T1G1V1N1O1N1S111G1A1F1G1Y1W1SV1R1D1K1S	179		
0Y	179	1G1V1E1G1E1D1M1A1R1G1N1N111H1Y1Q1A1T1E1Y1E1SS1Y1A1R1Y1A	222		
	1	11111111111111111111	1	11111111111111111111	11
Dib	180	GS1V1A1N1H1N1M1A1D1G1E1L111G1M1D1Y1A1V1E1Y1P1S1S1G1A1S1T1V1S	222		

RESULTS	t_b	STANDARD	PRT	197 AA
XYNA	58.10 ⁰⁰			
110	XYNA 58.10 ⁰⁰			
Ac	143.40 ⁰⁹			
Df	01 JUN 1974	(hr.), 29, (Treated)		

D1 01-JUN-1994 (rel. 2.9, last sequence update)
 D2 15-DEC-1998 (rel. 4.7, last annotation update)
 DE Endo 1,4-beta-xylanase A (E.C. 4.2.1.8) (Xylanase A) (1,4-beta-D-xylan
 GN xylanhydrolase A).
 D6 XNA.
 05 Schizophyllum commune (Bracket fungus).
 06 Eukaryota: Fungi: Basidiomycota: Hymenymycetes: *Homobasidiomycetes*:
 07 Stereum: Schizophyllaceae: Schizophyllum.
 08

EN
[1] *Journal of Polymer Science*, 1992, 29, 1997.
SEQUENCE:
RE STRAITS ACCT 38548 / PHENARZ
RE YAMUCHI M., Koy T., OJITO M., Watson D.C., Wakarink W.;
EN (In) Wisser J., Beldman G., Kusters van Smeulen M.A.,
RE Vanden A.G.J. (eds.);
EN Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).

- KN [2].
- KP SEQUENCE, AND DISULFIDE BONDS.
- KI STRAIN=ALCO 38548 / DELMAR.
- KJ METALINE=94063044 / PUBMED-8248466.
- KA Oki T., Roy C., Watson D.C., Makretchuk W., Campbell R., Yashchuk M., Juraszek J., Patco M.B.:
- RA "Amino acid sequence and thermostability of xylanase A from *Thermophilum* commune".
- RT PERS Lett. 334:296-300(1993).
- KL

RP PARTIAL SEQUENCE, AND ACTIVE SITE (OLD 87).
KC STRAIN ATCC 38548 / DEIMAR;
RX MEDLINE 94155888; PubMed 7906649;

KT "Identification of a glutamate residue at the active site of xylanase
 KT A from *Schizophyllum commune*."
 KL Eur. J. Biochem. 219:821-827 (1994).
 CR 1- FUNCTION: HYDROLYSES XYLANS INTO XYLOBIOSIS AND XYLASE. THIS
 CEC XYLANASE HAS A VERY BROAD PH ACTIVITY.

cc -1- CATALYTIC ACTIVITY: Endoglycopolys of 1,4 beta-D xylosidic
cc linkages in xylans.
cc
cc -1- PATHWAY: XILAN DEGRADATION.
cc
cc -1- SUBCELLULAR LOCATION: Secreted.
cc
cc -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY 6 (FAMILY 11 OF GLYCOSYL
cc HYDROLASES).

136 1.LR7: S48973; S48974;
137 1.LR7: A44597; A44597;
138 HSSP: 041097; 1YNA.
139 InterPro: IPR001137; Glyco_Hydro_11.
140 Pfam: PF00457; Glyco_Hydro_11; 1.
141 PRINTS: PR00911; GLYDCLASE1.
142 ProSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
143 ProSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KM	AVIN degradation:	HYDROLASE	GLYCOSYLASE
FT	ACT_SITE	87	NUCLEOPHILE (PROBABLY).
FT	ACT_SITE	184	PROTON DONOR (BY SIMILARITY).
FT	DISULFID	111	
SD	SDSEQUENCE	197 AA:	20978 MW: 4.28074567e-1 PHEV: 67e64:

Quincy Match	53.68	Score 663	1st 1	Length 177
Post Local Similarity	61.38	Prod. No. 1,2847		
Matches 197	Conservative	26	Mistakes	43
				67 cups

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
01	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
02	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
03	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
04	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
05	0																																																																																																				

[illegible]

DB 183 FEYUSSGATITV 196

RESULT 7

XYN2_MAGGR STANDARD: PRT: 213 AA.

AC P55335: Q01171:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-MAY-2000 (Rel. 39, Last annotation update)

DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)

DE (1,4-beta-D-xylan xylanohydrolase 22).

OS Magnaporthe oryzae (Rice blast fungus) (Pycnidaria grisea).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.

OX NCBI_TaxID:148405;

KN 111

RP SEQUENCE FROM N.A.

RX MEDLINE:96172742; PubMed:8589407;

RT Magnaporthe oryzae, the rice blast fungus.

RT Magnaporthe grisea, the rice blast fungus.

RL Mol. Plant Microbe Interact. 8:506-514(1995).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

linkages in xylans.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 1) OF GLYCOSYL

HYDROLASES).

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or send an email to license@isb-sib.ch).

CC EMBL: 147529; AAC41683.1;

DR HSSP: 041097; LYNA

DR InterPro: IP800117; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLYDRLASE11.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

DR Xylan degradation; Hydrolase; Glycosidase; Signal.

FT SIGNAL 1 39 POTENTIAL.

FT CHAIN 40 233 ENDO-1,4-BETA-XYLANASE 22.

FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).

FT ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).

SO SEQUENCE 233 AA; 25491 MW; 40096383658198 CRC64;

Query Match 53.3%; Score 660; DB 1; Length 233;

Best local Similarity 53.7%; Pred. No. 2,6e-47;

Matches 144; Conservative 36; Mismatches 59; Indels 12; Gaps 6;

DB 1 MVSFTVALAALATG:ALAPPA--GNAT-----ELEKROTPNSEKMHVYYSSWSOG 52

DB 1 MVSFTSLVTVAVAGSALAIPADCMKTCGPREQLMRKOSTPSTSRHNGYYSSWTDG 60

DB 53 GAQATYINLEGGYEISWQKGNVAGKGNPGLNARAIHFESVYGP--MNSYLAVYCW 110

DB 61 ASPOVQGNNGNSYSVQWQSGNFGVGRKGNMP--GSKSLIYSCTFN--VNNCNAVLCYCW 119

DB 111 TRNPLVEVYIVENFGYDPSSGATDLCVEGDGSIYRLGKTTKRVNAPSILGQIUTFWYWS 170

DB 120 TQNPILVEVYIENFGYDPSSGATDLCVEGDGSIYRLGKTTKRVNAPSILGQIUTFWYWS 179

DB 171 VRODKRTSGTVGTGCHFDIARAGLNVNGDHYVQIVAFIEYSSGVARITV 221

DB 180 IROKRNKSGTVNTGCFDAMERAGMRR--GNHMYIVATEGYSAGNSNIN 229

RESULT 8

XYN2_EMENI STANDARD: PRT: 221 AA.

AC P55335: Q01176:

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)

DE (1,4-beta-D-xylan xylanohydrolase 2).

OS *Emmericella nidulans* (*Aspergillus nidulans*).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; *Emmericella*.

OX NCBI_TaxID:5072;

KN 111

RP SEQUENCE FROM N.A.

RX MEDLINE:96286210; PubMed:8787417;

RT Perez-Gonzalez J.A., de Graaf L.H., Visser J., Ramon D.

RT Molecular cloning and expression in *Saccharomyces cerevisiae* of two

RT *Aspergillus nidulans* xylanase genes.

RL Appl. Environ. Microbiol. 62:2179-2182(1996).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

linkages in xylans.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 1) OF GLYCOSYL

HYDROLASES).

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or send an email to license@isb-sib.ch).

CC EMBL: 249893; CAA0074.1;

DR HSSP: 148793; LYNA.

DR InterPro: IP800117; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLYDRLASE11.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

DR Xylan degradation; Hydrolase; Glycosidase; Signal.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.

FT ACT_SITE 117 117 NUCLEOPHILE (BY SIMILARITY).

FT ACT_SITE 208 208 PROTON DONOR (BY SIMILARITY).

SO SEQUENCE 221 AA; 23517 MW; 42665E80DE9475 CRC64;

Query Match 51.5%; Score 637.5; DB 1; Length 221;

Best local Similarity 54.0%; Pred. No. 1,7e-45;

Matches 122; Conservative 36; Mismatches 59; Indels 9; Gaps 4;

DB 1 MVSFTVALAALATG:ALAPPA--GNAT-----ELEKROTPNSEKMHVYYSSWSOG 56

DB 1 MVSFTSLVTVAVAGSALAIPADCMKTCGPREQLMRKOSTPSTSRHNGYYSSWTDG 57

DB 57 TYNLEGGYEISWQKGNVAGKGNPGLNARAIHFESVYGP--MNSYLAVYCW 110

DB 58 TYNLEGGYEISWQKGNVAGKGNPGLNARAIHFESVYGP--MNSYLAVYCW 116

DB 117 EYIVENFGYDPSSGATDLCVEGDGSIYRLGKTTKRVNAPSILGQIUTFWYWS 176

DB 117 EYIVENFGYDPSSGATDLCVEGDGSIYRLGKTTKRVNAPSILGQIUTFWYWS 176

DB 177 TSGSVTQNHFIAMSDQGMTL--GTHNYQIVAVYGYSSNSASITVS 221

```

DE 01 OCT 1996 (REL. 34, created)
DE 01 OCT 1996 (REL. 34, last sequence update)
DE 01 NOV 1997 (REL. 35, last annotation update)
DE Find 1,4 beta xylanase 11 precursor (EC 3.2.1.8) (Xylanase 11)
DE (1,4-beta-D-xylan xylanohydrolase 11).
GN XYNM.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocommataceae; Mitosporic Trichocommataceae; Aspergillus-
OC NCH_TaxID-5061;
GN
RN
RN SEQUENCE FROM N.A.
RE STRAIN=FO 4066;
RA
RA Submitted (SEP 1994) to the EMBL/Genbank/DDBJ databases.
CC
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4 beta D xylotriose
CC linkages in xylans.
CC
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY 6 (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC
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CC or send an email to license@isb.ch).
CC
CC EMBL: D38071; BAA07265.1; -
CC HSRP: P09850; XNMB.
OR
OR InterPro: IPR00137; glyco_hydro_11.
OR TrnM: PF00457; glyco_hydro_11; 1.
OR PRINITS: PRO0071; GLABYDGLASE11.
OR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
OR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
OR Xylan degradation; hydrolase; glycosidase; signal.
PT
PT SIGNAL. 1 18
PT PROPEP 19 37
PT CTNIN 38 225
PT ACT_SITE 121 121
PT ACT_SITE 212 212
PT
PT SEQUENCE 225 AA; 24057 MW; C4HHH007ABZBHPD Ch064;
NO

```

DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
 OS Trichoderma harzianum
 OC Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; mitosporic Hypocreales; Trichoderma
 OX NCBI_TaxID=5544;
 RN [1]
 KP SEQUENCE
 KP STRAIN=F58;
 KA Yauchui M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
 KA Sadler J.N.;
 RT The amino acid sequence of the 20 kD xylanase from Trichoderma
 RT harzianum F58.*;
 RL (In) Visser J., Beljman G., Kusters-van Someren M.A.,
 RL Voragen A.G.J. (eds.);
 RN Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).
 RP [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 KA Campbell K.L., Rose D.R., Makarchuk W.W., To R.J., Song W.,
 KA Yauchui M.;
 RT High resolution structures of xylanases from *B. citroulans* and
 RT *T. harzianum* identify a new folding pattern and implications for the
 RT atomic basis of the catalysis.*;
 RL (In) Suominen P., Reluokainen T. (eds.);
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72.
 RL Foundation for Biotechnical and Industrial Fermentation Research,
 RL Helsinki (1993).
 RL Helstinki (1993).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR FDB: 1XND: 20-DEC-94.
 DR Interpro: IPRO01137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation: Hydrolase; glycosidase; 4D-structure.
 FT ACT_SITE 86 Nucleophile.
 FT ACT_SITE 177 PROTON DONOR.
 SO SEQUENCE 190 AA: 20703 MW: 64064 DIC35990698 CRO64;

Query Match 50.9%; Score 630.5; DB 1; Length 190;
 Best Local Similarity 60.2%; Pred. No. 5.5e-45;
 Matches 115; Conservative 27; Mismatches 48; Indels 1; Gaps 1;

YQ 32 QTPNSHGMHGYYSWMSDGAQATYTNLGGTYELSDGDNLVGKKNNGIARAI 91
 DB 1 QTIQPGTGYNSGYYSWMSDGAQATYTNLGGTYSNNSNPFYAGKGMQPGTKNKVI 60
 YQ 92 HFGGVQPNQNSYLAAYGWTNNLVEEYIVENEGTDFSSGADLCTVEGJSTYRLGKT 151
 DB 61 NFGSGYBNQNSYLSIYGSRNPLIEEYIVENEGTDFSSGADLCTVEGJSTYRLGKT 120
 YQ 152 TRNAPRSITGTFHGYWVRQDRKTSQTYGTGCHPAPARAGLNNNGHYVIVALEST 211
 DB 121 QRVNOPSIIIGTALFYQWVRKRNHRSQSVANTNHPNMAASHQTLT-GTMDYCIVAVEGY 179
 YQ 212 FSSGYARITVA 222
 DB 180 FSSGSASTVS 190

RESULT 12
 XYNB_STRLI
 ID XYNB_STRLI STANDARD; PRI: 335 AA.
 AC P26515;
 DT 01-NOV-1992 (Rel. 23, created)
 DT 16-OCT-2001 (Rel. 40, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)

DE (1,4-beta-D-xylan xylanohydrolase B).
 GN XYNB.
 OS Streptomyces lividans.
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;
 OC Actinomycetales; Streptomycineae; Streptomycesaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 KP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
 KP STRAIN=66 / 1326;
 RC MEDLINE=92077439; PubMed 1744521;
 RA Shareck F., Roy C., Yauchui M., Morosoli R., Kluepfel D.;
 RT *Sequences of three genes specifying xylanases in Streptomyces
 RT lividans.*;
 RL Gene 107:75-82(1991).
 RN [2]
 RP REVISIONS TO 29-42 AND 252-407.
 RP STRAIN=66 / 1326;
 RC MEDLINE=95186900; PubMed 7544741;
 RA Shareck F., Biely P., Morosoli R., Kluepfel D.;
 RT Analysis of DNA flanking the xlnB locus of Streptomyces lividans
 RT reveals genes encoding acetyl xylan esterase and the RNA component of
 RT ribonuclease P.*;
 RL Gene 153:105-109(1995).
 RN [3]
 RP REVISION TO 225.
 RA Shareck F.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
 CC COMPONENT OF PLANT CELL-WALLS. XLNA AND XYNB SEEM TO ACT
 CC SEQUENTIALLY ON THE SUBSTRATE TO YIELD XYLOBIOSE AND XYLOSE.
 CC AS CARBON SOURCES.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
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 CC or send an email to license@sib-sib.ch).
 CC EMBL: M64552; AAC06114.2; .
 DR HSP: P09850; 1XNB.
 DR Interpro: IPRO01137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation: Hydrolase; glycosidase; Signal.
 FT SIGNAL 1 41
 FT CHAIN 42 345 ENDO-1,4-BETA-XYLANASE B.
 FT DOMAIN 42 270 CATALYTIC.
 FT DOMAIN 231 249 LINKER ("HINGE") (GLY RICH BOX).
 FT DOMAIN 250 335 XILAN-BINDING (PENTANAL).
 FT ACT_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
 SO SEQUENCE 335 AA: 55575 MW: 51381458888400P CRO64;

Query Match 47.5%; Score 587.5; DB 1; Length 345;
 Best Local Similarity 51.5%; Pred. No. 3.4e-41;
 Matches 117; Conservative 24; Mismatches 73; Indels 14; Gaps 4;

YQ 6 PVAL-----AALATGALAFPAQATELERQTTPNSGCHDQYYYSWMSDGAQATY 58
 DB 14 PVLIVRSAMAVAIAMALMLP---GDAQDVIVTINQDCHNNYYYSFWDSQGVSM 70
 YQ 59 TINFGSTYELISWDGDNLVGKKNNGIARAIHFNAYGUPNNSYLAAYGWTNNLVEEY 118

DB 71 NMGSQVSTSWNTNENFVAKIKWANG - GRRFYQVSTSPNSGNALALVDMISNVEY 129
 QY 119 YVENEETVYSSGATDITETDSTLHMLKTEFVNANSLHLETOFPDQVSWPQIKRS 178
 DB 119 YVENEETVYSSGATDITETDSTLHMLKTEFVNANSLHLETOFPDQVSWPQIKRS 178
 DB 119 YVENEETVYSSGATDITETDSTLHMLKTEFVNANSLHLETOFPDQVSWPQIKRS 178
 QY 179 GVVQVDFEFAWAKAVLNNGHRYVQVVAEVEFSSGAKRTTVAWG 225
 DB 108 GLETFNHFAMAKAGMPLNFSYMIKMTVEYQSSSSSTVWGRTG 234
 RESULT 14
 XYNM_SURE1 STANDARD: PRT: 240 AA.
 AC P26220;
 DT 01 MAY 1992 (rel. 22, last sequence update)
 DT 01 MAY 1992 (rel. 22, last sequence update)
 DT 15 JUL 1999 (rel. 48, last annotation update)
 DE Bado 1,4 beta-xylanase c precursor (pI 3.2,1.8) (Xylanase c)
 DE (1,4 beta-D-xylan xylanhydrolase c).
 GN XYNM.
 OS Streptomyces lividans.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomyces; Streptomycesaceae; Streptomyces.
 OX NCBI TaxId 1916;
 RN 111
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 50-ND.
 RC STRAIN 66 / 126;
 RX MEDLINE 94077459; PubMed 1746921;
 RA Sharrock P., Roy C., Yamauchi M., Morosoli R., Kluepfel T.;
 RL "Sequences of three genes specifying xylanases in Streptomyces
 lividans.";
 RT Gene 107:76-82(1991).
 CC 1. FUNCTION: CONTRIBUTES TO HYDROLYSE HEMICELLULOSE, THE MAJOR
 CC COMPONENT OF PLANT CELL-WALLS.
 CC 2. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC 3. PATHWAY: XYLAN DEGRADATION.
 CC 4. SUBCELLULAR LOCATION: Secreted.
 CC 5. SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
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 CC or send an email to license@isb.sib.ch).
 DB EMBL: M64553; AAA26836.1;
 DB EMBL: A25407; CAA01768.1;
 DB PIR: J80591; J80591.
 DB HSSP: P09850; 1XNB.
 DB InterPro: IPRO01187; glyco_hydro_11.
 DB Pfam: PF00457; glyco_hydro_11;
 DB PRINTS: PR00911; GLYDRLASE1.
 DB PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DB PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; hydrolase; glycosidase; signal.
 FT SIGNAL 1 49
 FT CHAIN 50 240 EMBL 1,4-BETA-XYLANASE C.
 FT ACT SITE 144 144 NUCLEOPHILE (BY SIMILARITY).
 FT ACT SITE 226 226 PROTON DONOR (BY SIMILARITY).
 DB SQUENITE 240 AA; 256/3 MW: P56644578014274 C6864;
 QY 11 ALAAVFAVAF - ANMATELEKQITVNSERIMHRYVYSWSSGCAQATVIMLEATVET 68
 Post local similarity 44.6%; Score 540; DB 1; Length 240;
 Matched 119; Conserved 26; Mismatches 66; Indels 14; Gaps 5;
 11

DB 34 ALAAVFAVAF - ANMATELEKQITVNSERIMHRYVYSWSSGCAQATVIMLEATVET 68
 QY 69 SWGRKSNVGRKGMVGNVNAHLEVEYVQFNQNSYLAAYGCMINPVEYVENEYTD 128
 DB 69 SWGRKSNVGRKGMVGNVNAHLEVEYVQFNQNSYLAAYGCMINPVEYVENEYTD 128
 DB 69 SWGRKSNVGRKGMVGNVNAHLEVEYVQFNQNSYLAAYGCMINPVEYVENEYTD 128
 QY 88 GRTNAGNVAKQKQWGT - DKNVRYMVFNVGNVGTALYMTSNPLVEYTVNMSYR 145
 DB 88 GRTNAGNVAKQKQWGT - DKNVRYMVFNVGNVGTALYMTSNPLVEYTVNMSYR 145
 QY 129 PSSNPLATVETVSTVLAETKTRVNAVSTHQTQVQVSVQKRT SCVQVQGR 186
 DB 129 PSSNPLATVETVSTVLAETKTRVNAVSTHQTQVQVSVQKRT SCVQVQGR 186
 DB 129 PSSNPLATVETVSTVLAETKTRVNAVSTHQTQVQVSVQKRT SCVQVQGR 186
 QY 146 PE - GTFYGVSSGRTVDTVOTFRYNAVSHEKTFQVQVSVQKRTSISGTTGNH 204
 DB 146 PE - GTFYGVSSGRTVDTVOTFRYNAVSHEKTFQVQVSVQKRTSISGTTGNH 204
 QY 187 FFAWAKAGMNGHRYVQVVAEVEFSSGAKRTTVAWG 222
 DB 204 FFAWAKAGMNGHRYVQVVAEVEFSSGAKRTTVAWG 222
 RESULT 14
 XYNM_CHEP1 STANDARD: PRT: 644 AA.
 AC P54865;
 DT 01 OCT 1996 (rel. 44, created)
 DT 01 OCT 1996 (rel. 44, last sequence update)
 DT 16 OCT 2001 (rel. 40, last annotation update)
 DE Bado 1,4 beta-xylanase D precursor (pI 3.2,1.8) (Xylanase D) (XY11).
 GN XYNM.
 OS Cellulomonas fimi.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Micrococcales; Cellulomonadaceae; Cellulomonas.
 OX NCBI TaxId 1708;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN 221;
 RX MEDLINE 94224155; PubMed 8170199;
 RA Millward Sadler S.J., Poole D.M., Hollissat R., Hazlewood G.P.;
 RA Clarke J.H., Gilbert R.J.;
 RT "Evidence for a general role for high-affinity non-catalytic
 RT cellulose binding domains in microbial plant cell wall hydrolases.";
 RL Mol. Microbiol. 11:375-382(1994).
 CC 1. FUNCTION: END/ACTING XYLANASE WHICH DISPLAYS NO DEFECTABLE
 CC ACTIVITY AGAINST POLYSACCHARIDES OTHER THAN XYLAN. HYDROLYSES
 CC GLUCOSIDIC BONDS WITH RETENTION OF ANEMERIC CONFIGURATION.
 CC 2. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC 3. PATHWAY: XYLAN DEGRADATION.
 CC 4. SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
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 CC or send an email to license@isb.sib.ch).
 DB EMBL: X76729; CAA54145.1;
 DB HSSP: P09850; 1XNB.
 DB InterPro: IPRO01919; CHO 2.
 DB InterPro: IPRO01187; glyco_hydro_11.
 DB InterPro: IPRO02509; Polysac_deact.
 DB Pfam: PF00554; CHO 2; 2.
 DB Pfam: PF00457; glyco_hydro_11; 1.
 DB Pfam: PF01522; Polysac_deact; 1.
 DB PRINTS: PR00911; GLYDRLASE1.
 DB PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DB PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW hydrolase; glycosidase; signal; repeat.
 FT SIGNAL 1 44
 FT CHAIN 44 644 EMBL 1,4-BETA-XYLANASE D.
 FT DOMAIN 44 240 CATALYTIC.
 FT DOMAIN 241 245 LINKER ("HINER") (GLY RICH BOX).
 FT DOMAIN 246 644 2 X 88 AA APPROXIMATE CHO-LIKE REPEATS.
 FT REPEAT 246 444 1.

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OM protein - protein search, using SW model

Run on: April 27, 2002, 18:35:51 ; Search time 74.8 Seconds

(Without alignment)
520.372 Million cell updates/sec

Title: US-09-115-660-2

Perfect score: 128
Sequence: 1 MCGFPVAMIAIATGALAF.....VATESYSSQYAKIIVAVWG 225

Scoring table: BLAST/MS62
Gapop 10.0 , Gapext 0.5

Searched: 56222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 56222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_ornanelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	965	77.9	194	P81536	Paecilomyces
2	821.5	66.4	227	Q90V23	Q90V23 helminthosp
3	785	63.4	295	Q9C1R2	Q9C1R2 fusarium ox
4	775.5	62.6	227	Q00263	Q00263 ascochyta p
5	716.5	57.9	231	Q13447	Q13447 cochlidiobol
6	701.5	56.7	231	Q00350	Q00350 cochlidiobol
7	692.5	55.9	227	Q9HCE1	Q9HCE1 humicola gr
8	691.5	55.9	219	Q12579	Q12579 chaetomium
9	689	55.7	241	Q12580	Q12580 chaetomium
10	684.5	55.3	223	Q02244	Q02244 trichoderma
11	676.5	54.6	241	Q9C1R1	Q9C1R1 fusarium ox
12	671.5	54.2	224	Q99015	Q99015 trichoderma
13	660.5	53.4	221	P87037	P87037 aspergillus
14	659	53.2	232	Q9HFA4	Q9HFA4 aspergillus
15	638	51.5	290	Q9HEZ0	Q9HEZ0 phanerochaete
16	638	51.5	290	Q9HEY9	Q9HEY9 phanerochaete

17	632.5	51.1	223	Q90VP9	Q90VP9 trichoderma
18	610.5	49.4	223	Q9H-PH0	Q9H-PH0 pentactin
19	599.5	48.4	223	Q90U02	Q90U02 pentactin
20	585.5	47.3	335	Q9RKN6	Q9RKN6 streptomyces
21	579	46.8	283	Q96UV7	Q96UV7 pentactin
22	573	46.3	228	Q59962	Q59962 streptomyces
23	573	46.3	338	Q56265	Q56265 thermomonos
24	563	45.5	335	Q9R0M4	Q9R0M4 cellulosoma
25	562.5	45.4	335	Q9R0B8	Q9R0B8 streptomyces
26	562.5	45.4	335	Q08346	Q08346 streptomyces
27	561	45.3	329	Q9RKH9	Q9RKH9 streptomyces
28	557.5	45.0	191	Q9EM89	Q9EM89 streptomyces
29	554.5	44.8	241	Q9R172	Q9R172 streptomyces
30	553	44.7	240	Q56013	Q56013 streptomyces
31	541	43.7	216	Q74716	Q74716 claviceps p
32	528	42.6	661	Q59674	Q59674 pseudomonas
33	517.5	41.8	129	Q92245	Q92245 marnefella
34	505.5	40.8	210	Q9KEP3	Q9KEP3 bacillus ba
35	498	40.2	656	Q59400	Q59400 cellulosoma
36	481.5	38.9	211	Q54993	Q54993 actinomyces p
37	474	38.3	461	Q52475	Q52475 candida hol
38	470.5	38.0	213	Q59254	Q59254 bacillus su
39	470.5	38.0	217	Q97402	Q97402 phaeoan. cor
40	469.5	37.9	213	Q59256	Q59256 bacillus sp
41	467.5	37.8	213	Q92B36	Q92B36 bacillus sp
42	462	37.4	212	Q9E9B9	Q9E9B9 penicillium
43	452	36.5	354	Q9RC94	Q9RC94 bacillus sf
44	452	36.5	354	Q59257	Q59257 bacillus sp
45	448.5	36.2	120	Q90U04	Q90U04 ascochyta 1

ALIGNMENTS

RESULT 1					
P81536					
ID P81536	PRELIMINARY:	PRT:	194 AA.		
AC P81536:					
DT 01-JUN-2000 (TrEMBLrel. 14, Created)					
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)					
DT 01-JUN-2000 (TrEMBLrel. 17, Last annotation update)					
DE KMD-1.4-BETA-XYLANASE (EC 3.2.1.8) (XYLANASE) (1.4-BETA-D-XYLAN XYLANOXYLASE) (DX) (FRAGMENT).					
OS Paecilomyces variotii.					
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;					
OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Paecilomyces.					
OX NCBI_TaxId:45996;					
RN [1]					
RP X-RAY CRYSTALLOGRAPHY (1.59 ANGSTROMS), AND PARTIAL SEQUENCE.					
RC STRAIN-BANKING:					
RX MEDLINE-20000955; PubMed-10623548;					
RA Kumar P.R., Eswaramoorthy S., Vithayathil P.J., Viswanatha M.A.;					
RT "The tertiary structure at 1.59 A resolution and the proposed amino acid sequence of a family-11 xylanase from the thermophilic fungus Paecilomyces variotii bacter.;"					
RI J. Mol. Biol. 295:581-593(2000).					
RL - CATALYTIC ACTIVITY: ENDXYLANOLYSIS OF 1,4 BETA-D XYLANS.					
CC LINKAGES IN XYLANS.					
CC -1- PATHWAY: XYLAN DEGRADATION.					
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).					
CC HSSP: 043097; 1YNA.					
DR InterPro: IPR001147; Glyco_hydro_11.					
DR Pfam: PF00457; Glyco_hydro_11; 1.					
DR PRINIS: PR00911; GLYCOLASE11.					
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.					
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.					
KW Xylan degradation; Hydrolase; Glycosidase; Acetylation.					
FT MGN_TER 1 1					
FT MOD_RES 1 1					
FT ACT_SITE 86 86					
FT ACT_SITE 178 178					
FT DISULFID 110 154					

FT	194	194
NO. TIR		
SO	194 AA	20947 MM
SEQUENCE		

Query Match	77.98;	Score	965;	DB	4;	Length	194;
Post Local Similarity	87.68;	Prod. No.	1,10-66;				
Matches	169;	Conservative	11;	Mismatches	13;	Indels	0;
						Gaps	0;

[illegible]

```

RESULT      2
Q9UVZ3
ID          Q9UVZ3
PRELIMINARY;
PRC:       227 AA

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147 01 MAY 2000 (TREMOR-1, 13, created)
148 01 MAY 2000 (TREMOR-1, 13, last sequence update)
149 01 DEC 2001 (TREMOR-1, 19, last annotation update)
150 XYLAMASE: PREPITROR-1

```

035 Helminthosporiium turcicum.
04 Plakoyotolol; Plunol; Ascomycolol; Helminthosporiium
05 Moll Taxol 94612;

10	CONFORMATION OF THE NUCLEIC
11	ACID
12	SERIALS II.2:
13	Impey, Y., Paulin, L., Perathoner, J., Ambrose, P. S., &
14	"Cloning, sequencing and expression of a xylan-

RE: SUOMI (1994 (MAY 1999)) TO THE EMBL/GENBANK/DBI databases
EMBL; A12488.5; C2652417.1;
DDB; 044097; YNA.
Indet (1994 (1999))

DR
PRINTS; PRO00911; C:\HYDRIASE\11.
DR
PROSITE; P800776; GLYCOSYL_HYDROL_P11_1; 1.
DR
PROSITE; P800777; GLYCOSYL_HYDROL_P11_2; 1.

PT	20	2.27	XYLANASE.
SEQUENCE	2.7 AA:	24124 MW:	BA864075EELS06E 0'80'64

Best Local Similarity	67.7%	Prod. No. 1.40-55;
Matches	154;	Conservative
	25;	Mismatches
	41;	Indels

1 MVSFSTLTAAVATCAAAATPDLAAAPSIDAAKSTNTEPTNMGCTYSWWSIQRAR 60

116 VEVYLVENETLYDSSGATLALIVETDSYRLAKTRVNPSTLDTQTDFQYWSVRLQK 175

07 176 RRSCTVOTGCHFDWAKRATLNNNDHRYQIVATEGYFSSGSARITV 22
180 KSSGSVMNKTHERDAMASKGMNL QSHYYQIVATEGYFSSGSASITV 224

RESULT	3
Q9C1R2	
ID	Q9C1R2
PRELIMINARY	
PRT	295 AA

PT 01-JUN-2001 (TREMblrel, 17, (created))
PT 01-JUN-2001 (TREMblrel, 17, last sequence update)
PT 01-DEC-2001 (TREMblrel, 19, last annotation update)
XLANASE 5 PROTEIN.

05 Fusarium oxysporum f. sp. lycopersici,
06
07 Hyphomycetes; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes,
08
09 Hyphomycetes; mitospores; Hyphomycetes; Fusarium,
0X NCBI_TaxID 59765;

RT Fusarium oxysporum f. sp. lycopersici^a?

DR
EMBL: AF246830; AAC27794.1;
HISSP: 043097; LYNA.
DR
InterPro: IPR01137; glyco_hydro..1.
DR
PRINTS: PR00411 (GLYDRIASE1)
OR

DR PROSTATE: F500777; GLYCOSYL-HYDROL, F11-Z; 1-
SEQUENCE: 295 AA; 30858 MW; CAA41056.DD3C104 C*6064

Best Local Similarity 64.98; Prod. No. 1.20 52;
Matches 146; Conservative 40; Mismatches 45; Indels 4; Gaps 3

1 MWHFTSVFAGLSTVAGSLAAFSKKEGLFSKIKRAGTINSSQTNMPEYYSWWSHRCADATY 60

119 Y I V E N E N G I Y O P S S A T I H A T T E C H O N S I Y K I G K T I K V N A N S I D E T O F I D O Y W S V R Q D K E T S I D H

[illegible]

RESULT 4

PT	01-Nov-1996	(TtEMBLrel_01, created)
PT	01-Nov-1996	(TtEMBLrel_01, last sequence update)
PT	01-Dec-2001	(TtEMBLrel_19, last annotation update)

06 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
07 Dothideales; Didymella
08 NCBI_TaxID=47971;
09

RT "Molecular cloning and DNA sequencing of a xylanase gene from the phytopathogenic fungus *Ascochyta blight*":

PMR: δ 6.88 (9H, s, C_6H_9); 4.12 (2H, t, CH_2); 1.2 (3H, t, CH_3).

Query Match	55, 98;	Score 692.5;	DB 3;	Length 227;
Best Local Similarity	56.6M;	Prod. No. 1.1e 45;		
Matches 128;	Conservative 29;	Mismatches 62;	Indels 7;	Gaps 3

RESULT	B
C12579	
ID	C12579
AC	C12579;
LOC	01-INV-1996, (T-EMUL-01, T-Feat ed)
LIT	01-INV-1996, (T-EMUL-01, Last sequence updated)
LIT	01-INV-2000, (T-EMUL-01, 19, Last annotation updated)
DE	EMUL-BEATL-4, XYLANASE A (EC 4.2.1.B).

Courtesy Matt C.
F5, JM; Secore G91, b; LH 3; Lanthanum, etc.

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RESULT      9
Q12580
ID      Q12580
PRELIMINARY;
PRI;      241 AA.

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50 SEQUENCE 241 AA; 25564 MW; 10C1D4B012Z72F777E CR64

KE:SHI, T 10
Q002244


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Db 1 MVSFNSLVAVSAATCALAPPEFHNGIHVEPROSTPAIGTINNGYFNSPWTHKAGSVTY 60
QY 59 TLEGGTYELSMGDDGNLVKGGKMPALNARALHFEYVYQPNNGSYLAAYGWTRNPLEY 118
Db 61 NNGPAGHYSVTWGNADNFVAGKGNPG-SAGALSTANYOPNGNSYLSYQWSINPLEY 119
QY 119 YIVENFGTYNDSSGATDLAGTVEGDSYVRIQKTRVNAPSTRTGTFIDYWSYKDKRTS 178
Db 120 YILEDFGTYNPAVSLTHKGTITSDGATYDVEYEGTRVNEPSTOGTATPNOYWSLESSKRSS 179
QY 179 GTVOTGCHTAMARAGLINVNGIRHYQIVATEGCFSSGATATVAIWG 225
Db 180 GTVTANHFAMKOLGFLP-GTFNYQIVATEGYSSSSSTVTVNPAQ 225

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Search completed: April 27, 2002, 18:43:58
 Job time: 487 sec

